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OM nucleic - nucleic search, using sw model

Run on: September 4, 2004, 07:47:42 ; Search time 9619 Seconds
(without alignments)
17239.884 Million cell updates/sec

Title: US-09-927-091-3
Perfect score: 3826
Sequence: 1 aggtgcgtggaccgaagc.....aaaaaaaaaaaaaaaaaaaa 3826

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 3470272 seqs, 21671516995 residues

Word size : 18

Total number of hits satisfying chosen parameters: 31322

Minimum DB seq length: 2500
Maximum DB seq length: 5000

Post-processing: Listing first 45 summaries

Database :

GenEmbl.*

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- 39: em_htgo_hum.*
- 40: em_htgo_mus.*
- 41: em_htgo_other.*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	3826	100.0	3826	6	AX491279	Sequence
2	3163	82.7	3436	6	AX877131	Sequence
3	3163	82.7	3436	6	BD156501	Primer fo
4	3163	82.7	3436	9	AK001621	Homo sapi
5	3014	78.8	3259	9	BC001222	Homo sapi
6	3014	78.8	3259	9	BC007999	Homo sapi
7	3014	78.8	3259	9	BC011689	Homo sapi
8	3014	78.8	3259	9	BC012152	Homo sapi
9	2994	78.3	3243	6	AX775831	Sequence
10	2631	68.8	3148	9	AK122896	Sequence
11	119	3.1	3216	10	BC049095	Mus muscu
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17	26	0.7	2955	10	BC021442	Mus muscu
18	26	0.7	3270	9	BC050552	Homo sapi
19	26	0.7	4059	10	BC056981	Mus muscu
20	26	0.7	4798	10	BC056365	Mus muscu
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22	25	0.7	2539	9	BC013285	Homo sapi
23	25	0.7	2562	10	AY292400	Mus muscu
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28	25	0.7	2645	8	CGL012164	Casuarina
29	25	0.7	2663	5	BC053915	Danio rer
30	25	0.7	2756	3	AF132159	Drosophil
31	25	0.7	2771	9	BC014276	Homo sapi
32	25	0.7	2772	3	AY051427	Drosophil
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34	25	0.7	2836	10	AY112739	Rattus no
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37	25	0.7	2965	10	AY112738	Rattus no
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ALIGNMENTS

RESULT 1	AX491279	AX491279	3826 bp	DNA	linear	PAT 16-AUG-2002
LOCUS	Sequence 3 from Patent WO0212285.					
DEFINITION	AX491279					
ACCESSION	AX491279.1	GI:22323980				
VERSION						
KEYWORDS						
SOURCE						
ORGANISM						
	Homo sapiens (human)					
	Homo sapiens					
	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;					
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
REFERENCE						
AUTHORS	Killary, A., Chandler, D. and Lott, S.					
TITLE	The tumor suppressor car-1					
JOURNAL	Patent: WO 0212285-A 3 14-FEB-2002;					

Pred. No. is the number of results predicted by chance to have a

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FEATURES		Location/Qualifiers		1..3826		/organism="Homo sapiens"		/mol_type="unassigned DNA"		/db_xref="taxon:9606"	
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ORIGIN											
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Matches 3826; Conservative		0; Mismatches 0; Indels 0; Gaps 0;									
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DB	61	CCAGGTTTGGGCGCGGATCCGGAGCTGACGGGCGGGGACCCCTCTCTCTCTCTGTC	120								
QY	121	GCTACAGCCATGTAAGCTCGGCTGGCTGCTGCCCTCCCTCCAGGATTCGCCATCCCA	180								
DB	121	GCTACAGCCATGTAAGCTCGGCTGGCTGCTGCCCTCCCTCCAGGATTCGCCATCCCA	180								
QY	181	GCTTCTCGCCCTCCCGGACCGCCCGCCACCCCGGGATTTGACCCCTTTAAGGGTCCAC	240								
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DB	541	GCGCGCGCTCTCTACGCGCGCCCTGCGCTGCGGCGCCCTCTCTGCTGCGGCTGCG	600								
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DB	1081	CTTAAGCGACAACCTGCGGAGACCAAGTCTTCCACAAAGAGCTCGGAGCCTATTCGCG	1140								
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DB	1321	GACCGGACACCTCTGCTGCGGTGGCTCACTGTCTCGAGCGGCTCAAGGAAAAATC	1380								
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DB	1381	CATGAGACCAACCTCACATATGAAGACTTCCGAGCTCCCAAGTACACAGCGCCCTGCGAG	1440								
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DB	1501	GACCGGCGCACAGCCACCGAGCGCTGATCTCTGCGAGCTGACACCATTTGGCTTAC	1560								
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DB	1861	CTGGACTATGACCAAGGCTTGTCTCATCTTCTCAATGTGATGACATGTCTGGCTCTAC	1920								
QY	1921	ACCTTCCGCGAAGGATTCCTGCAAGCTCTGCTCTTACTTCAAGCTGCGCAGAGCCAC	1980								
DB	1921	ACCTTCCGCGAAGGATTCCTGCAAGCTCTGCTCTTACTTCAAGCTGCGCAGAGCCAC	1980								
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ORIGIN

Query Match		82.7%; Score 3163; DB 6; Length 3436;
Best Local Similarity		99.9%; Pred. No. 0;
Matches 3433; Conservative 0; Mismatches 3; Indels 1; Gaps 1;		
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DB	1	CCACTACCTCTAGATGCCCTCCCGGGCTGGGTCCACGGAGTCTCAGCCGCGCACCCC 60
QY	430	TTCTCGGCTTACCTTCCTCCGACAGCACCCCTCCCTTCTCGGTAGCTCCTACCCC 489
DB	61	TTCTCGGCTTACCTTCCTCCGACAGCACCCCTCCCTTCTCGGTAGCTCCTACCCC 120
QY	490	TGCTGTGGGGCTGTCCCGCGCCGACGCTCGGTGCTGCTCCGACAGCGCGCGC 549
DB	121	TGCTGTGGGGCTGTCCCGCGCCGACGCTCGGTGCTGCTCCGACAGCGCGCGC 180
QY	550	TCTCTCAGCGCCCTCGCCCTCGGGCCCTCTCTGCTGCGCCCTGGCGCATGGCG 609
DB	181	TCTCTCAGCGCCCTCGCCCTCGGGCCCTCTCTGCTGCGCCCTGGCGCATGGCG 240
QY	610	TGCAGCTCAAGAGAGAGCTGTGTCTCATCTGCTCAGCATCTACAGGACCCGGTG 669
DB	241	TGCAGCTCAAGAGAGAGCTGTGTCTCATCTGCTCAGCATCTACAGGACCCGGTG 300
QY	670	AGCTGGGTGAGAGACTACTTCTCGCGCGCTGATCAGGAGACTGGGTGGCGGAG 729
DB	301	AGCTGGGTGAGAGACTACTTCTCGCGCGCTGATCAGGAGACTGGGTGGCGGAG 360
QY	730	GAGGCGCAGGGCGCCGCGACTGCCCGAGTGGCGGCGACGTTCCCGAGCCGCGCTG 789
DB	361	GAGGCGCAGGGCGCCGCGACTGCCCGAGTGGCGGCGACGTTCCCGAGCCGCGCTG 420
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QY	910	TGCTCAGGACGCGCGCTTCTGTCTTCTTGGGACGAGCTGCACTGCAACGAGCAG 969
DB	541	TGCTCAGGACGCGCGCTTCTGTCTTCTTGGGACGAGCTGCACTGCAACGAGCAG 600
QY	970	CATCAGGTCAACGGCATCGACGCGCTTCGACGAGCTGACAGGGAGTGAAGGACCAA 1029
DB	601	CATCAGGTCAACGGCATCGACGCGCTTCGACGAGCTGACAGGGAGTGAAGGACCAA 660
QY	1030	CTTCAGGCTTCAAGACAGGAGCGGACACACGAGCGCTGAGCTGCTCAAGCGA 1089
DB	661	CTTCAGGCTTCAAGACAGGAGCGGACACACGAGCGCTGAGCTGCTCAAGCGA 720
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DB	721	CAACTGGGAGACCAAGTCTTCCACCAAGAGCTGCGGACCACTATCGGCGAGGCTTC 780
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QY	1210	GACACGCGCCGACACGCTGACGACATCGAGCAGAAAGTCCAGCGTCTACAGCCAGCAGCTG 1269
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QY	1390	AACTCTACATATGAAGACTTCCCGACCTCCAAAGTACACAGGCCCCCTGCAGTACACCATC 1449
DB	1021	AACTCTACATATGAAGACTTCCCGACCTCCAAAGTACACAGGCCCCCTGCAGTACACCATC 1080
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DB	1081	TGGAAGTCCCTGTTCCAGGACATCCACCCAGTGCAGCGCCCTTAACCTTGACACCGGCG 1140
QY	1510	ACAGCCACACAGCGCTGATCTCTGCGAGACTGCACCATTTGGCTTACGGAACACTTG 1569
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QY	1570	CACCCACAGCCACTGCAGACTCGCCAAAGCGCTTCGATGTGGAGGTGTGGTGTGGGT 1629
DB	1201	CACCCACAGCCACTGCAGACTCGCCAAAGCGCTTCGATGTGGAGGTGTGGTGTGGGT 1260
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DB	1261	TCTGAAGCCTTCACTAGTGGGTCCACTACTGCGAGGTGGTGGCGGAGAGACCCAG 1320
QY	1690	TGGGTGATCGGCTGACACAGGCGGCAAGCGGAGGCGAGCATCCAGATCCAGCCC 1749
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DB	1681	ACAACCTTCTGGACCACTGCGACCTGCAAGAGCCCTGCCAGG-AGATAGAGAGACTGG 1739
QY	2110	ACTCCAGCCACCGTGGCCACTGGAGACCTCAGGCGAGTTGTTTACCTCCAGCCCTCCAG 2169
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QY	2170	TCTGTAATGAGAGTTGATTCCTTCTTCTTAACTCTTTCAGCATCGATGTTCTG 2229
DB	1800	TCTGTAATGAGAGTTGATTCCTTCTTCTTAACTCTTTCAGCATCGATGTTCTG 1859
QY	2230	TAGCTCTGACCTTGATAGGATACAGCTTTGATCCAGAGTGTGACATGGCTTCTCCTCA 2289
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Best Local Similarity 99.9%; Pred. No. 0;
Matches 3433; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

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QY	430	TTCTCTCGGTTTACCTCTCTTCGGGACAGACCCCTCCCTTCTCCGTTAGTCTCTACCCC	489
DB	61	TTCTCTCGGTTTACCTCTCTTCGGGACAGACCCCTCCCTTCTCCGTTAGTCTCTACCCC	120
QY	490	TGCTCTGTCGGGCTCTGTCCTCCGGCGCCAGCCCTCGTGTGCTTCCGACAGCGCCGGC	549
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QY	610	TGCAGCTCAAGGACGAGTCTGTGCTGCATCTGCCTGAGCACTACAGGACCCGGT	669
DB	241	TGCAGCTCAAGGACGAGTCTGTGCTGCATCTGCCTGAGCACTACAGGACCCGGT	300
QY	670	AGCTTGGCTCGAGCACTACTTCTCGCGCGCTGCATCAGGAGCACTGGGTGCGGAG	729
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DB	421	GCGCCCAAGCTCAAGCTGGCCAACTCGTGGAGCGCTACAGTCTCTTCGGCTGGAGCC	480
QY	850	ATCCTCAACG	909
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QY	910	TGCTCAGCAGCAGCGCGCTTCTCTGTTCTTCTGGACGAGCTGCACTGCGAGCAG	969
DB	541	TGCTCAGCAGCAGCGCGCTTCTCTGTTCTTCTGGACGAGCTGCACTGCGAGCAG	600
QY	970	CATCAGTCAACGGCATCGACGCGCTTCGACGAGCTGCAGAGGGAGCTGAAGACCA	1029
DB	601	CATCAGTCAACGGCATCGACGCGCTTCGACGAGCTGCAGAGGGAGCTGAAGACCA	660
QY	1030	CTTCAGGCCCTTCAAGCAGCAGCGGGAAACAACAAGCGCTGCACTGCTCAAGCGA	1089
DB	661	CTTCAGGCCCTTCAAGCAGCAGCGGGAAACAACAAGCGCTGCACTGCTCAAGCGA	720
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DB	721	CAACTGGCGGAGACCAAGTCTTCACCAAGCGCTGGGACCACTATCGCGGAGCGCTTC	780
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ACCESSION AK001621
VERSION AK001621.1 GI:7022986
KEYWORDS oligo capping; fis (full insert sequence).
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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1
Isoqai,T., Ota,T., Hayashi,K., Sugiyama,T., Otsuki,T., Suzuki,Y.,
Nishikawa,T., Nagai,K., Sugano,S., Ishibashi,T., Fujimori,K.,
Tanai,H., Kinata,M., Watanabe,M., Hiraoka,S., Ishii,S., Kawai,Y.,
Salto,K., Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagahara,K.,
Masuo,Y. and Kanehori,K.
NEDO human cDNA sequencing project
Unpublished
2 (bases 1 to 3436)
Isoqai,T. and Otsuki,T.
Direct Submission
Submitted (16-FEB-2000) Takao Isoqai, Helix Research Institute,
Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
(E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
NEDO human cDNA sequencing project supported by Ministry of
International Trade and Industry of Japan; cDNA full insert
sequencing: Research Association for Biotechnology; cDNA library
construction, 5'- & 3'-end one pass sequencing and clone selection:
Helix Research Institute (supported by Japan Key Technology Center
etc.) and Department of Virology, Institute of Medical Science,
University of Tokyo.
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ACCESSION		BC001222	
VERSION		BC001222.1	GI:12654758
KEYWORDS		MGC.	
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ORGANISM		Homo sapiens	
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
AUTHORS		Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
		1 (bases 1 to 3259)	
		Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,	
		Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,	
		Altschul, S.F., Zeeberg, B.S., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,	
		Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,	
		Datchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,	
		Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,	
		Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,	
		Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,	
		Abramson, R.D., Mullany, S.J., Bosak, S.A., McEwan, P.J.	
		McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,	
		Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,	
		Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,	
		Fahy, J., Helton, E., Kettman, M., Madan, A., Young, A.C., Shvchenko, Y.,	
		Sanchez, A., Whiting, M., Madan, A., Touchman, J.W., Green, E.D.,	
		Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,	
		Dickson, M.C., Rodriguez, A.C., Greenwood, J., Schmutz, J., Myers, R.M.,	
		Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalusz, D.E.,	
		Schneerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.	
		Generation and initial analysis of more than 15,000 full-length	
		human and mouse cDNA sequences	
		Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)	
JOURNAL		22388257	
MEDLINE		12477932	
PUBMED		2	(bases 1 to 3259)
REFERENCE		Strausberg, R.	
AUTHORS		Direct Submission	
TITLE		Submitted (11-DEC-2000) National Institutes of Health, Mammalian	
JOURNAL		Gene Collection (MGC), Cancer Genomics Office, National Cancer	
		Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,	
		USA	
REMARK		NIH-MGC Project URL: http://mgc.nci.nih.gov	
COMMENT		Contact: MGC help desk	
		Email: cgabbs@mail.nih.gov	
		Tissue procurement: ATCC	
		cDNA Library Preparation: Rubin Laboratory	
		cDNA Library Arranged by: The I.M.A.G.E. Consortium (LLNL)	
		DNA Sequencing by: Genome Sequence Centre,	

BC Cancer Agency, Vancouver, BC, Canada
info@bcgsc.bc.ca

Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,
Leticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo
Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven
Ness, Pawan Pandoh, Anna-liisa Prabhu, Parvaneh Saedi, Jacqueline
Schein, Duane Smalius, Michael Smith, Lorraine Spence, Jeff Stott,
Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,
George Yang, Scott Zuyderduyn, Marco Marra.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LINL at: <http://image.llnl.gov>
Series: iFAL Plate: 6 Row: j Column: 17
This clone was selected for full length sequencing because it
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FEATURES

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ORIGIN

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 ACCESSION
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 VERSION
 BC007999.1
 GI:14124949
 KEYWORDS
 MGC.

SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 3259)
AUTHORS	Strausberg,R.L., Feigold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.P., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carinci,P., Frange,C., Rana,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullaly,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Kettner,M., Madan,A., Rodrigues,S., Sanchez,A., Whitting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smalilus,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
MEDLINE	22388257
PUBMED	12477932
REFERENCE	2 (bases 1 to 3259)
AUTHORS	Strausberg,R.
TITLE	Direct Submission
JOURNAL	Submitted (15-MAY-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
REMARK	NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT	Contact: MGC help desk Email: cgabbs-remail.nih.gov Tissue Procurement: ATCC cDNA Library Preparation: Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILLNL) DNA Sequencing by: Genome Sequence Centre, BC Cancer Agency, Vancouver, BC, Canada info@bcsc.bc.ca Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Leticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline Schein, Duane Smalilus, Michael Smith, Lorraine Spence, Jeff Scott, Michael Thorne, Miranada Tsai, Natasha van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.
FEATURES	<p>Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILLNL at: http://image.llnl.gov</p> <p>Series: IPAL Plate: 23 Row: a Column: 20.</p> <p>Location/Qualifiers</p> <p>1..3259</p> <p>/organism="Homo sapiens"</p> <p>/mol_type="mRNA"</p> <p>/db_xref="taxon:9606"</p> <p>/clone="MGC:15757 IMAGE:3357436"</p> <p>/tissue_type="Eye, retinoblastoma"</p> <p>/clone_lib="NIH_MGC_16"</p> <p>/lab_host="DH10B-R"</p> <p>/note="Vector: pOTB7"</p> <p>1..3259</p> <p>/gene="FLJ10759"</p> <p>/db_xref="LocusID:55223"</p> <p>34..1461</p> <p>/codon_start=1</p> <p>/product="hypothetical protein FLJ10759"</p> <p>/protein_id="AAH07999.1"</p>
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VERSION BC011689
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REFERENCE 1 (bases 1 to 3259)
          Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
          Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
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          Scherch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
          Generation and initial analysis of more than 15,000 full-length
          human and mouse cDNA sequences
          Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
          Strausberg,R.
          Direct Submission
          Submitted (30-JUL-2001) National Institutes of Health, Mammalian
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          USA

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REMARK  NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT  On Dec 19, 2003 this sequence version replaced gi:15079757.
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          Email: cgaaps@email.nih.gov
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          DNA Sequencing by: National Institutes of Health Intramural
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          Web site: http://www.nisc.nih.gov/
          Contact: nisc_mgc@nhgri.nih.gov
          Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
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REFERENCE
AUTHORS
1 (bases 1 to 3259)
Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
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Spletten,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
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Fahey,J., Helton,E., Kettman,M., Madan,A., Rodriguez,S.,
Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smalusz,D.E.,
Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
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2 (bases 1 to 3259)
Strausberg,R.
Direct Submission
Submitted (02-AUG-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA

REMARK
COMMENT
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgabs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@bcgsc.bc.ca

Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,
Leticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo
Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven
Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline
Schein, Duane Smalusz, Michael Smith, Lorraine Spence, Jeff Scott,
Michael Thorne, Miranada Teai, Natasja van den Bosch, Jill Vardy,
George Yang, Scott Zuyderduyn, Marco Marra.

Clone distribution: MGC clone distribution information can be found
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RESULT 9
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LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE

AX775831 3243 bp mRNA linear PAT 14-JUL-2003
 Sequence 101 from Patent WO03048202.
 AX775831
 AX775831.1 GI:32693549

Homo sapiens (human)
 Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
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Matsuda, A. and Muramatsu, S.

NF-KB activating gene
 Patent: WO 03048202-A 101 12-JUN-2003;

Asahi Kasei Kabushiki Kaisha (JP)
 Location/Qualifiers

FEATURES

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AK122896
AK122896.1 GI:34528340
oligo capping: fis (full insert sequence).
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ORGANISM
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Ota, T., Nakagawa, S., Senoh, A., Mizuguchi, H., Inagaki, H.,
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Takahashi-Fujii, A., Oshima, A., Sugiyama, A., Kawakami, B., Suzuki, Y.,
Sugano, S., Nagahari, K., Masuho, Y., Nagai, K. and Isogai, T.
NEDO human cDNA sequencing project
Unpublished
2 (bases 1 to 3148)
Isogai, T. and Yamamoto, J.
Direct Submission
Submitted (15-JUL-2003) Takao Isogai, FLJ Project (HRI Team); 2-6-7
Kazusa-Kamatari, Kisarazu, Chiba 292-0818, Japan
(E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
NEDO human cDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan; cDNA full insert sequencing:
Research Association for Biotechnology (RAB); cDNA library
construction: Helix Research Institute (HRI) (supported by Japan
Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,
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Evaluation; clone selection for full insert sequencing: HRI and
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VERSION BC049095.1 GI:29294764
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ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 3216)
Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shennan, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raja, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalios, D.E., Schnerch, A., Schein, J.B., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

JOURNAL MEDLINE
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL
REMARK
COMMENT
FEATURES
source
gene
CDS
misc_feature
misc_feature
misc_feature
misc_feature
ORIGIN

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
2238257
12477932
2 (bases 1 to 3216)
Strausberg, R.
Direct Submission
Submitted (19-MAR-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgaps-remail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
cDNA Library Preparation: M. Bento Soares, University of Iowa
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: University of Iowa, Dr. M. Bento Soares and Dr.
Thomas L. Casavant.
Web site: http://genome.uiowa.edu
Contact: bento-soares@uiowa.edu; tom-casavant@uiowa.edu
Bonaldo, M.F., Akabogu, I., Bair, T., Bair, J., Crouch, K., Davis, A.,
Fishler, K., Keppel, C., Kucaba, T., Lebeck, M., Melo, A., Schaefer, K.,
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Casavant, T., Soares, M.B.
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
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1072. 1410
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DB	19	GCCTCTGGCCATGGCTGAGCTCAAGGACGAGCTGCTGTGCTCCATCTGCTGAGC 78
QY	652	ATCTACGAGGACCCGCTGAGCTGGCTGCGAGCACTACTTCTGCGCGCTGATCAC 710
DB	79	ATCTACGAGGACCCGCTGAGCTGGCTGCGAGCACTACTTCTGCGCGCTGATCAC 137
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LOCUS	AK125034	3444 bp mRNA linear PRI 09-SEP-2003
DEFINITION	Homo sapiens cDNA FLJ43044 fis, clone BRTHA3003474.	
ACCESSION	AK125034	
VERSION	AK125034.1 GI:34530992	
KEYWORDS	oligo capping; fis (full insert sequence).	
SOURCE	Homo sapiens (human)	
ORGANISM	Homo sapiens	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.	
AUTHORS	Ota, T., Nakagawa, S., Senoh, A., Mizuguchi, H., Inagaki, H., Sugiyama, T., Irie, R., Orsuki, T., Sato, H., Wakanatsu, A., Ishii, S., Yamamoto, J., Isono, Y., Kawai-Hio, Y., Saito, K., Nishikawa, T., Kimura, K., Yamashita, H., Matsuo, K., Nakamura, Y., Sekine, M., Kikuchi, H., Kanda, K., Wagatsuna, M., Murakawa, K., Kanehori, K., Takahashi-Fujii, A., Oshima, A., Sugiyama, A., Kawakami, B., Suzuki, Y., Sugano, S., Nagahari, K., Masuho, Y., Nagai, K. and Isogai, T.	
TITLE	NEDO human cDNA sequencing project	
JOURNAL	Unpublished	
REFERENCE	2 (bases 1 to 3444)	
AUTHORS	Isogai, T. and Yamamoto, J.	
TITLE	Direct Submission	
JOURNAL	Submitted (15-JUL-2003) Takao Isogai, FLJ Project (HRI Team); 2-6-7 Kazusa-Kamatari, Kisarazu, Chiba 292-0818, Japan	
COMMENT	NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan key Technology Center etc.); 5' and 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: HRI and RAB.	
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CDS		
ORIGIN	2.6%; Score 99; DB 9; Length 3444;	
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Matches 99; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	
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Db	2715	CAGAGGAGCTGAAGACCACTTCAGGCCCTTCAAGACAGCGAGCGGACACACCGAA	2655
QY	1069	CGCTGCGAGCTGCTCAAGCGACCAACTGGCGGAGACCAAG	1107
Db	2655	CGCTGCGAGCTGCTCAAGCGACCACTGGCGGAGACCAAG	2617
RESULT 13			
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LOCUS	BC060625	4150 bp	mRNA linear ROD 12-NOV-2003
DEFINITION	Mus musculus Tnf receptor-associated factor 2, mRNA (cDNA clone IMAGE:6831932), partial cds.		
ACCESSION	BC060625		
VERSION	BC060625.1 GI:38197727		
KEYWORDS	Mus musculus (house mouse)		
SOURCE	Mus musculus		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus		
REFERENCE	1 (bases 1 to 4150)		
AUTHORS	Klausner, R.L., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullaby, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butlerfield, Y.S., Krzywinski, M.I., Skalska, U., Smalley, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.		
TITLE	human and mouse cDNA sequences		
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)		
MEDLINE	22388257		
PUBMED	12477932		
REFERENCE	2 (bases 1 to 4150)		
AUTHORS	Strausberg, R.		
TITLE	Direct Submission		
JOURNAL	Submitted (31-OCT-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA		
REMARK	NIH-MGC Project URL: http://mgc.nci.nih.gov		
COMMENT	Contact: MGC help desk Email: cgabbs-remail.nih.gov Tissue Procurement: Dr. Jim Lin, University of Iowa cDNA Library Preparation: M. Bento Soares, University of Iowa cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: University of Iowa, Dr. M. Bento Soares and Dr. Thomas L. Casavant. Web site: http://genome.uiowa.edu Contact: Bento-soares@uiowa.edu; tom-casavant@uiowa.edu Bonaldo, M.F., Akabogu, I., Bair, T., Bair, J., Crouch, K., Davis, A., Fiebler, K., Keppel, C., Kucaba, T., Lebeck, M., Melo, A., Schaefer, K., Scheetz, T., Smith, C., Snir, E., Tack, D., Trout, K., Walters, J., Casavant, T., Soares, M.B.		
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov			
Series: Plate: Row: Column: 0			
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Db 4111 AGATGTCACAAAAAAGAAAAAAGAAAAA 4137

RESULT 14
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LOCUS HSM803417 4685 bp mRNA linear PRI 13-MAY-2003
DEFINITION Homo sapiens mRNA; cDNA DKFZp313H168 (from clone DKFZp313H168).
ACCESSION AL832110
VERSION AL832110.1 GI:21732653
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 4685)
AUTHORS Wambutt,R., Heubner,D., Mewes,H.W., Weil,B., Amid,C., Osanger,A.,
Fobo,G., Han,M. and Wiemann,S.
TITLE Direct Submission
JOURNAL Neuherberg, GERMANY
COMMENT Submitted (13-MAY-2003) MIPS, Ingolstaedter Landstr.1, D-85764
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by AGOWA (Berlin/Germany) within the cDNA sequencing
consortium of the German Genome Project.
This clone (DKFZp313H168) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further
information about the clone and the sequencing project is available
at http://mips.gsf.de/proj/cDNA/.

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Db 4656 AGATGTCACAAAAAAGAAAAAAGAAAAA 4682

RESULT 15
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LOCUS BC019375 2619 bp mRNA linear ROD 04-OCT-2003
DEFINITION Mus musculus DNA segment, Chr 1, ERATO Doi 622, expressed, mRNA

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BC019375
VERSION BC019375.1 GI:18043921
KEYWORDS MGC.
SOURCE Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 2619)
AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
Hopkins,R., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
Scheetz,T.E., Brownstein,M.J., Ustin,T.B., Toshiyuki,S.,
Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
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Fahey,J., Helton,E., Kettelman,M., Madan,A., Rodriguez,S.,
Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smallos,D.E.,
Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
22388257
12477932
REFERENCE 2 (bases 1 to 2619)
AUTHORS Strausberg,R.
TITLE Direct Submission
JOURNAL Submitted (19-DEC-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT Contact: MGC help desk
Email: cgaps-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 41 Row: k Column: 6
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ORIGIN

Query Match 0.7%; Score 26; DB 10; Length 2619;
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Db 2583 GATGTCAAAAAAAAAAAAAAAAAAAA 2608

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Job time : 9627 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 4, 2004, 06:55:12 ; Search time 944 Seconds
(without alignments)
17217.803 Million cell updates/sec

Title: US-09-927-091-3

Perfect score: 3826

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Scoring table: OLIGO NUC

Gapop_60.0, Gapext 60.0

Searched: 3373863 seqs, 2124099041 residues

Word size: 18

Total number of hits satisfying chosen parameters: 22942

Minimum DB seq length: 2500

Maximum DB seq length: 5000

Post-processing: Listing first 45 summaries

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- 1: Geneseqn1980s:*
- 2: Geneseqn1990s:*
- 3: Geneseqn2000s:*
- 4: Geneseqn2001as:*
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- 7: Geneseqn2003as:*
- 8: Geneseqn2003bs:*
- 9: Geneseqn2003cs:*
- 10: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	3163	82.7	3436	4	Aah14509 Human cDN
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4	26	0.7	4702	7	Abx76356 Lung canc
5	25	0.7	2522	2	Aav82781 Clone df3
6	25	0.7	2522	6	Abq92018 Human pol
7	25	0.7	2586	9	Adb62721 Human cDN
8	25	0.7	2629	5	Aah34824 Human col
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10	25	0.7	2647	5	Abv25449 Human pro
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15	25	0.7	3858	9	Adb59641 Human REM
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18	25	0.7	4498	8	Ada38053 DNA relat
19	25	0.7	4572	6	Abq98201 Human ost
20	25	0.7	4585	4	Ab115850 Drosophil
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25	25	0.7	4740	6	ABK50046 cDNA enco
26	25	0.7	4740	6	ABK83766 Human cDN
27	25	0.7	4740	7	ABZ96848 Human nuc
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30	24	0.6	2509	3	Aac78146 Human can
31	24	0.6	2512	9	AdE87242 Human pan
32	24	0.6	2558	4	ABL21586 Drosophil
33	24	0.6	2612	4	AAD05059 Human sec
34	24	0.6	2612	7	ADA56044 Gene enco
35	24	0.6	2612	7	ADA39854 Human sec
36	24	0.6	2633	4	AAL35789 Human mus
37	24	0.6	2633	7	ABX58777 cDNA enco
38	24	0.6	2642	4	ABL10304 Drosophil
39	24	0.6	2645	7	ABX63799 Human cDN
40	24	0.6	2661	7	ABZ18582 Group III
41	24	0.6	2677	4	AAI18016 Coniothyr
42	24	0.6	2690	6	ABA93708 Human tra
43	24	0.6	2720	4	AAH18311 Human cDN
44	24	0.6	2723	4	ABL27612 Drosophil
45	24	0.6	2820	3	AAA23433 cDNA enco

ALIGNMENTS

RESULT 1
ABK12806
ID ABK12806 standard; cDNA; 3826 BP.
XX
AC ABK12806;
XX
DT 18-JUN-2002 (first entry)
XX
DE Human cDNA encoding tumour suppressor CAR-1.
XX

Human; ss; tumour suppressor; gene; CAR-1; cytostatic; cancer; tumour; gene therapy; brain cancer; lung cancer; liver cancer; kidney cancer; colon cancer; stomach cancer; breast cancer; endometrial cancer; prostate cancer; testicular cancer; ovarian cancer; skin cancer; head and neck cancer; oesophageal cancer; bone marrow cancer; chromosome 1p31-1p36.
XX
OS Homo sapiens.
XX

Key Location/Qualifiers
CDS 604..2031
FT /*tag= a
FT /product= "CAR-1"
FT
WO200212285-A2.
XX
14-FEB-2002.
XX
09-AUG-2001; 2001WO-US025269.
XX
10-AUG-2000; 2000US-0225033P.
XX
23-AUG-2000; 2000US-0227560P.
XX
(TEXA) UNIV TEXAS SYSTEM.
XX
Killary A, Chandler D, Lott S;
XX
WPI; 2002-269088/31.
XX
P-PSDB; AAU78657.
XX
New tumor suppressor CAR-1 polypeptides and polynucleotides, useful for diagnosing cancer, for altering the phenotype of a tumor cell, for treating cancers or as a diagnostic or prognostic indicator of cancer.
XX
Claim 2; Page 134-135; 185pp; English.
XX

CC The invention relates to an isolated polynucleotide encoding a
 CC polypeptide being tumour suppressor, CAR-1. Also included are fragments
 CC of the polynucleotide from 15-5000 nucleotides, fragments of the protein
 CC from 10-50 amino acids, an expression cassette comprising the
 CC polynucleotide under the control of a promoter operable in eukaryotic
 CC cells, a method for suppressing growth of a cancer cells by contacting
 CC the cells with the expression cassette (i.e. gene therapy), a cell
 CC comprising the expression cassette, an anti-CAR-1 monoclonal or
 CC polyclonal antibody, a hybridoma cell that produces the monoclonal
 CC antibody, a method of diagnosing a cancer by assessing the expression of
 CC CAR-1 tumour suppressor in the cells of a tissue sample from a subject,
 CC methods for altering the phenotype of a tumour cell, methods for treating
 CC a subject with cancer by administering the tumour suppressor CAR-1 and a
 CC promoter active in eukaryotic cells, where the promoter is operably
 CC linked to the region encoding the tumour suppressor, a non-human
 CC transgenic eukaryote lacking a functional CAR-1 gene, a non-human
 CC transgenic eukaryote that over-expresses CAR-1 as compared to a similar
 CC non-transgenic eukaryote, a method of screening a candidate substance for
 CC anti-tumour activity by contacting a cell lacking functional CAR-1
 CC polypeptide, with a candidate substance and determining the effect of the
 CC candidate substance on the cell, an anti-tumour composition produced by
 CC contacting a cell lacking functional CAR-1 polypeptide, with a candidate
 CC substance, determining the effect of the candidate substance on the cell,
 CC identifying a candidate inhibitor substance, and making a composition and
 CC an isolated and purified nucleic acid that hybridizes, under high
 CC stringency conditions, to a DNA segment comprising about 15-3826 bases of
 CC the CAR-1 cDNA. The polynucleotide is useful for diagnosing cancer, for
 CC altering the phenotype of a tumour cell, for treating cancers (e.g.
 CC cancer of the brain, lung, liver, kidney, lymph node, pancreas, small
 CC intestine, blood cells, colon, stomach, breast, endometrium, prostate,
 CC testicle, ovary, skin, head and neck, oesophagus, bone marrow, blood, or
 CC other tissues), and as a diagnostic or prognostic indicator of cancer.
 CC CAR-1 may also be used in screening compounds for activity in either
 CC stimulating CAR-1 activity, overcoming the lack of CAR-1 or blocking the
 CC effect of mutant CAR-1 molecule. The gene for CAR-1 is located on
 CC chromosome 1 (1p31-1p36). The present sequence is the cDNA encoding CAR-1
 XX
 SQ Sequence 3826 BP; 797 A; 1286 C; 999 G; 744 T; 0 U; 0 Other;

Query Match 100.0%; Score 3826; DB 6; Length 3826;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 3826; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AGGCTGCGTGTGACACGAGCGGTGCTGTAAGCTCGCGGGGTAAAGGGTGGCGCTGGG 60
 DB 1 AGGCTGCGTGTGACACGAGCGGTGCTGTAAGCTCGCGGGGTAAAGGGTGGCGCTGGG 60
 QY 61 CCAGGGTTGGGGCCGGATCCGGAGCTGAGCGGCGCGCACCCCTCTCTCTCTGCC 120
 DB 61 CCAGGGTTGGGGCCGGATCCGGAGCTGAGCGGCGCGCACCCCTCTCTCTCTGCC 120
 QY 121 GGTACAGCCAAATGTACGGCTCGGCTGCGCTCCCTCCCGAGATTCCTCCATCCCA 180
 DB 121 GGTACAGCCAAATGTACGGCTCGGCTGCGCTCCCTCCCGAGATTCCTCCATCCCA 180
 QY 181 GGTCTCGGCTCCCGGACCGCCCGCCACCCCGGATTTGACGCCCTTAAAGGGTCCAC 240
 DB 181 GGTCTCGGCTCCCGGACCGCCCGCCACCCCGGATTTGACGCCCTTAAAGGGTCCAC 240
 QY 241 CCGGCTCCGGATCCCTTCTCCAGCTCTATCCCTTAGGACTGCCCCGCCCTTAGAA 300
 DB 241 CCGGCTCCGGATCCCTTCTCCAGCTCTATCCCTTAGGACTGCCCCGCCCTTAGAA 300
 QY 301 CTTCCCGCTCAGGATCTCGTCCCTCAGCGCTTCACAGCTCTCTCCAGCGCCATCGCC 360
 DB 301 CTTCCCGCTCAGGATCTCGTCCCTCAGCGCTTCACAGCTCTCTCCAGCGCCATCGCC 360
 QY 361 TTGAGTGGCCACTACTCTAGACTGCTCCCGGCTGGCGTCCACGAGTCTCAGCC 420
 DB 361 TTGAGTGGCCACTACTCTAGACTGCTCCCGGCTGGCGTCCACGAGTCTCAGCC 420
 QY 421 GCGCACCCCTTCTCTCGGTTACCTCTCTCCGACAGCACCCCTCTCTCTCGGTAGC 480

DB 421 GCGCACCCCTTCTCTCGGTTACCTCTCTCCGACAGCACCCCTCTCTCTCGGTAGC 480
 QY 481 TCTTACCCCTGCTGTGCGGGCTCTGTCGCGCGCCAGCCCTGGTGTCTCTCCGACA 540
 DB 481 TCTTACCCCTGCTGTGCGGGCTCTGTCGCGCGCCAGCCCTGGTGTCTCTCCGACA 540
 QY 541 GCGCGGCTCTCTCAGCGCCCTCTGCGCTCGGCGCCCTCTCTCTCTGTCGCCCTGGC 600
 DB 541 GCGCGGCTCTCTCAGCGCCCTCTGCGCTCGGCGCCCTCTCTCTCTGTCGCCCTGGC 600
 QY 601 GCGTGTGCTGTGCAAGGACGAGCTGTGTGTCTCTCTCTCTCTCTCTCTCTCTCTCT 660
 DB 601 GCGTGTGCTGTGCAAGGACGAGCTGTGTGTCTCTCTCTCTCTCTCTCTCTCTCTCT 660
 QY 661 GACCGGTGAGCTGGCTGTGAGCACTACTTCTGCGCGCTCTCTCTCTCTCTCTCTCTCT 720
 DB 661 GACCGGTGAGCTGGCTGTGAGCACTACTTCTGCGCGCTCTCTCTCTCTCTCTCTCTCT 720
 QY 721 GTGCGGACGAGGCGCGGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGG 780
 DB 721 GTGCGGACGAGGCGCGGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGG 780
 QY 781 CCGCGCTGCGGCGGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGG 840
 DB 781 CCGCGCTGCGGCGGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGG 840
 QY 841 CTGACGCACTCTCTCAGCGCGGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTG 900
 DB 841 CTGACGCACTCTCTCAGCGCGGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTG 900
 QY 901 AAGCTCTTCTGCTCAGCGGCGGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 960
 DB 901 AAGCTCTTCTGCTCAGCGGCGGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 960
 QY 961 CACGAGCAGCATAGGTCAACGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGG 1020
 DB 961 CACGAGCAGCATAGGTCAACGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGG 1020
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 DB 1021 AAGNCACTCTCAGCGGCTTCAAGACAGCGGCGGCAACACCGAAGCGCTGCGGCTGCGG 1080
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 DB 1081 CTCAAGCGCAACTCTGCGGAGACCAAGTCTTCCACCAAGAGCTGCGGCTGCGGCTGCGG 1140
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 DB 1141 GAGGCTTCTGAGCGGCTGCAACGCGGCTGCTGTGAGCGGCAAGGCTGCTGAGGAG 1200
 QY 1201 CTGAGGCGGACACGCGCGGCTGACCGGCTGAGCGGCTGAGCGGCTGAGCGGCTGAGCG 1260
 DB 1201 CTGAGGCGGACACGCGCGGCTGACCGGCTGAGCGGCTGAGCGGCTGAGCGGCTGAGCG 1260
 QY 1261 CAGCAGCTGCGCAAGGCTCCAGGAGGAGCCAGATCTCTGAGGAGCGGCTGCTGAGGAG 1320
 DB 1261 CAGCAGCTGCGCAAGGCTCCAGGAGGAGCCAGATCTCTGAGGAGCGGCTGCTGAGGAG 1320
 QY 1321 GACCGGCAACCTCTCTGCTGGGTGGCTCACTGTCTGAGGAGCTCAAGGAGGAGGAG 1380
 DB 1321 GACCGGCAACCTCTCTGCTGGGTGGCTCACTGTCTGAGGAGCTCAAGGAGGAGGAG 1380
 QY 1381 CATGAGACCACTCAGCATATGAAGTCTCCGAGCTCTCAAGTACAGCGGCTCTGAGGAG 1440
 DB 1381 CATGAGACCACTCAGCATATGAAGTCTCCGAGCTCTCAAGTACAGCGGCTCTGAGGAG 1440
 QY 1441 TACACCATCTGGAAGTCTCTGTTCCAGGACATCCACCCAGTGCAGCGGCTTAAACCTG 1500
 DB 1441 TACACCATCTGGAAGTCTCTGTTCCAGGACATCCACCCAGTGCAGCGGCTTAAACCTG 1500
 QY 1501 GACCGGCGACAGCCCAACGAGCGCTGATCTCTGCGGAGCTGACCACTGTTGGCTTAC 1560

Db 1501 GACCGGGCACAGCCACACAGCGCCTGATCTGTGGAGCACTGCACCACTTGTGGCTTAC 1560
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Db 1621 GTGCTGGGTTCCTGAAGCCCTTCAGTAGTGGCGTCCACTACTCTGGAGAGTGGTGGCGGAG 1680
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Db 1681 AAGACCCAGTGGGTGATCGGGGTGGCACAGAAAGCGCGAAGCGCGAGCGCATCCAG 1740
QY 1741 ATCCAGCCAGCGCGGCTTCTACTGCATCGTGATGCAGATGGCAACCACTACAGCGC 1800
Db 1741 ATCCAGCCAGCGCGGCTTCTACTGCATCGTGATGCAGATGGCAACCACTACAGCGC 1800
QY 1801 TGCACGGAGCCCTTGCACGGCGCTTAACGTCCGGGACAAGCTTGACAAGGTGGGTGCTTTC 1860
Db 1801 TGCACGGAGCCCTTGCACGGCGCTTAACGTCCGGGACAAGCTTGACAAGGTGGGTGCTTTC 1860
QY 1861 CTGGACTATGACCAAGGCTTGCTCTCTCTCAATGCTGATGACATGTCTGGCTCTAC 1920
Db 1861 CTGGACTATGACCAAGGCTTGCTCTCTCTCAATGCTGATGACATGTCTGGCTCTAC 1920
QY 1921 ACCTTCCGGGAGAAGTTCCCTGGCAAGCTCTGCTCTTACTTCAAGCCCTGGCCAGAGCCAC 1980
Db 1921 ACCTTCCGGGAGAAGTTCCCTGGCAAGCTCTGCTCTTACTTCAAGCCCTGGCCAGAGCCAC 1980
QY 1981 GCCAATGGCAAGACCTTCAGCGCTCGGGATCAACACCGTCGGCATCTAGTCCAGGCAG 2040
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QY 2041 AAGGAGACCAACCTCTCTGGGACCACTGCCACTGCAAGAGCCCTGCCAGGAAGATAG 2100
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Db 2161 AGCCTCCAGTCTGTAATAATGGAGTTGCATTCCTACTTCTTAAACTCTCTTCCAGCATC 2220
QY 2221 GATGTTCTGAGTCTGACCTTGATAGGATACAGCTTTGATCCCAAGATGTGACATGGC 2280
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Db 2281 TTCTCCTCAGGGCAACCCCTGCGCACCTCATCCCATCTTCTCAGGGCGAGGGACTA 2340
QY 2341 CTTCCAGTGTCTCCCTCCAGCCCAAGCCCTGACCTCAGGAAGTGTCCAGACATGGCCAGT 2400
Db 2341 CTTCCAGTGTCTCCCTCCAGCCCAAGCCCTGACCTCAGGAAGTGTCCAGACATGGCCAGT 2400
QY 2401 AGTTGACGCCGGAAGACACACAGACCCCTCTTATGTCCCATGGCTAAGACTTACCCC 2460
Db 2401 AGTTGACGCCGGAAGACACACAGACCCCTCTTATGTCCCATGGCTAAGACTTACCCC 2460
QY 2461 TGACCAAGCTAGTAGTGGGCCATTTACCTTGACCCCTGACAGTGGTCAAGTAGT 2520
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Db 2521 ACCTGCTCTAGGTTGCTGAGAGCAACCTCTCTCGCCACCCCAACCAAGAACTAT 2580
QY 2581 ATGGTTCCTACTTCTCCCACTGATCTGCTGGTCAAGTATGCTGTGGCCTGTGGAAG 2640
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QY 2641 CACCTGGTAGTTGAGTCCACACATTATAGTATGTGCGCACCACTTCTCTGCGCCACAGGCC 2700
Db 2641 CACCTGGTAGTTGAGTCCACACATTATAGTATGTGCGCACCACTTCTCTGCGCCACAGGCC 2700
QY 2701 GAGGACAGGGTGAAGGTATACCCAAAGCTGATGACAGAGCCCACTTASCCCTAAAGCAACT 2760
Db 2701 GAGGACAGGGTGAAGGTATACCCAAAGCTGATGACAGAGCCCACTTASCCCTAAAGCAACT 2760
QY 2761 GAGGACAGAGCTCCCTGAGTATCGAGTCCCGAGTAGCTCTGAACAAGAGTCCAGCCA 2820
Db 2761 GAGGACAGAGCTCCCTGAGTATCGAGTCCCGAGTAGCTCTGAACAAGAGTCCAGCCA 2820
QY 2821 ACCCTCTTCAGCAGCAGCCCTCTGTGACCTGAGGTGACAGGAGCTTCCAGAGCAGTTG 2880
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QY 2881 TTGTAATTAGGACCCCAAGCACTGGGAGGGGCTGTTGGCTAGACCCCTTGTCAAGCTTGGC 2940
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Db 3541 TTTCTTTCTAGTCTTGGGGCTAGATTCGTGACTTTGGGTCTCTGACACAACACACCATC 3600
QY 3601 CCAAGTAGTCCGGAAGAGCTAAACAGGGGTCTTAAATGGCTGCCCGCCACCCG 3660
Db 3601 CCAAGTAGTCCGGAAGAGCTAAACAGGGGTCTTAAATGGCTGCCCGCCACCCG 3660
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Db 3661 GGCCTCCCTTGGGCAAAAGGAATTTGTAGCCCTTACCCCAACCTTCACTACAGAACT 3720

1390 AACCTCACATATGAAGACTTCCGAGCTCCAGTACACAGGCCCTCGAGTACACCATC 1449
1021 AACCTCACATATGAAGACTTCCGAGCTCCAGTACACAGGCCCTCGAGTACACCATC 1080
1450 TGAAGTCCCTGTTCCAGGACATCCACCAGTCCAGCGCCCTAAACCTTGGACCCGGGC 1509
1081 TGAAGTCCCTGTTCCAGGACATCCACCAGTCCAGCGCCCTAAACCTTGGACCCGGGC 1140
1510 ACAGCCCAACAGCGCTGATCTCTGTCGAGGACTGCACCATGTGTGCTTACGCAACTTG 1569
1141 ACAGCCCAACAGCGCTGATCTCTGTCGAGGACTGCACCATGTGTGCTTACGCAACTTG 1200
1570 CACCCACAGCCTAGCAGGACTCGCCAAAGCGCTTCGATGTGAGGTGTCGGTCTGGGT 1629
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1441 CCTTGAACCGGGTTAAAGTTCGGGCAAGCTTTGAACAAGTGGGTGTCTTCTTGGACTAT 1500
1870 GACCAAGGCTGCTCATCTTCTACATGTGTATGATGTCATGCTCGCTCTACACCTTCCGC 1929
1501 GACCAAGGCTGCTCATCTTCTACATGTGTATGATGTCATGCTCGCTCTACACCTTCCGC 1560
1930 GAGAACTTCCCTGGCAAGCTCTGCTCTTACTTACGCCCTGGCCAGACCAAGCAATGGC 1989
1561 GAGAACTTCCCTGGCAAGCTCTGCTCTTACTTACGCCCTGGCCAGACCAAGCAATGGC 1620
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2050 ACACCTCTCTGGGACCACTGCCACCTGCAAGACCTGCCAGGAGATAGAAGCTGG 2109
1681 ACACCTCTCTGGGACCACTGCCACCTGCAAGACCTGCCAGG-AGAAGAAGACCTGG 1739
2110 ACTCCAGCCCAACCGTGGCCACTGGAGACCTCAGGCCAGTTGTTTACCTCCAGCCTCCAG 2169
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2100 TAGTGATGGGCCATTATACCTTGGACCCAGTCCACAGTGTGTACAGGTAGTACCTGGTCC 2159
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2280 GTTGAAGTCCACACATTATATAGTCACTGTCACCACTTCTCTGCCACAGGCCCGAGGACAG 2339
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2700 CTGAATTTCCAGAACTCCAGCGCCAGATTCAATCATGCTGTTGTGACACAGAAAGCTG 2759
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2880 GTTCCCAAACTTAAATTTTACAGAGATCTGTTTGGGGGAACTTAAGTCAGATCCAGA 2939
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2940 ACCTTGGCTGCAAGGAGTCTGGGAAATGTCTATCTCCCTAGAGAGAAAGTTAGGCTGGTG 2999
3370 GAGCAAGCCCACTCGCTGTTTTTCTGCCACAGCATCCAATCGTGAAGAACTCGGGAGAGG 3429
3000 GAGCAAGCCCACTCGCTGTTTTTCTGCCACAGCATCCAATCGTGAAGAACTCGGGAGAGG 3059
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3060 GTGGAGTCCACATATAGGGTGTCTGCCCCCTTGGCTCTATCTCCCTGCCAGAGCTGGGAA 3119
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3120 CTGGAGGATGGGCTGCAAGACTGAGCCCTAAATGTCTCCCGGCTTGACTTTCTTTCT 3179
3550 AGTCTCTGGGCTCTAGATTCTGCACTTGGGCTCTCTGACACAAACACACCATCCCAAGTAG 3609

Db 3180 AGTCCTGGGGCTAGATTCTGCACTTGGGGTCTCTGACACACACACATCCCAAAGTAG 3239
 QY 3610 CCGAAGAGCTAAACACAGGGGGTCTTAAATGGCTGCCCGCCACCCGGGGCTCCCT 3669
 Db 3240 CCGAAGAGCTAAACACAGGGGGTCTTAAATGGCTGCCCGCCACCCGGGGCTCCCT 3299
 QY 3670 TGGCAAAAGAAATGTGAGCCCTTACCCCAACCCCTTCAACTTACAGAAATCTGGGCCACCC 3729
 Db 3300 TGGCAAAAGAAATGTGAGCCCTTACCCCAACCCCTTCAACTTACAGAAATCTGGGCCACCC 3359
 QY 3730 CAGCAGTATTTTATTTAAATGTTGGCCATTTATGAGTTATGATCAATTTGATTAAA 3789
 Db 3360 CAGCAGTATTTTATTTAAATGTTGGCCATTTATGAGTTATGATCAATTTGATTAAA 3419
 QY 3790 TTTAAAGTTACAGATGTC 3806
 Db 3420 TTTAAAGTTACAGATGTC 3436

RESULT 3
 ID ADC37268
 XX ADC37268 standard; DNA; 3243 BP.
 AC ADC37268;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 DE Nuclear factor kappa B (NF-kappaB) activating gene, SEQ ID 101.
 XX
 KW Nuclear factor kappa B; NF-kappaB, inflammation; autoimmune disease;
 KW cancer; infectious disease; bone disease; AIDS;
 KW neurodegenerative disease; ischaemic disorder; Antiinflammatory;
 KW Immunomodulator; Cytostatic; Antimicrobial; Osteopathic; Anti-HIV;
 KW Neuroprotective; Nootropic; Cardiant; Gene therapy; human; gene; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO2003048202-A2.
 XX
 PD 12-JUN-2003.
 XX
 PF 03-DEC-2002; 2002WO-JP012644.
 XX
 PR 03-DEC-2001; 2001JP-00368692.
 PR 05-DEC-2001; 2001US-0335829P.
 PR 03-OCT-2002; 2002JP-00291302.
 PR 04-OCT-2002; 2002US-0415769P.
 XX
 PA (ASAH) ASAHI KASEI KK.
 XX
 PI Matsuda A, Muramatsu S;
 XX
 DR WPI; 2003-505282/47.
 DR P-PSDB; ADC37269.
 XX
 PT New purified protein that activates nuclear factor kappa B (NF-kappaB),
 PT useful for treating inflammation, autoimmune diseases, cancers,
 PT infectious diseases, bone diseases, AIDS, neurodegenerative diseases or
 PT ischemic disorders.
 XX
 PS Claim 4; SEQ ID NO 101; 938pp; English.
 XX
 CC The present invention relates to novel proteins and their coding
 CC sequences (ADC37168-ADC37455), which activate nuclear factor kappa B (NF-
 CC kappaB). The proteins and their coding sequences are useful for treating
 CC a disease associated with NF-kappaB activation, such as inflammation,
 CC autoimmune diseases, cancers, infectious diseases, bone diseases, AIDS,
 CC neurodegenerative diseases, or ischaemic disorders.
 XX
 SQ Sequence 3243 BP; 715 A; 1023 C; 863 G; 642 T; 0 U; 0 Other;

Query Match 78.3%; Score 2994; DB 9; Length 3243;
 Best Local Similarity 99.9%; Pred. No. 0;

Matches 3234; Conservative 0; Mismatches 0; Indels 2; Gaps 2;
 QY 571 CCTCGGGCCCCCTCTCTGCTGGCCCTGCGGCATGCGCTGACGCTCAAGAGACGAGCTG 630
 Db 10 CCTCGGGCCCCCTCTCTGCTGGCCCTGCGGCATGCGCTGACGCTCAAGAGACGAGCTG 69
 QY 631 CTGTGCTCCATCTCTGCTGAGCATCTACAGGACCCGCTGAGCCTTGGCTGCGACACTAC 690
 Db 70 CTGTGCTCCATCTCTGCTGAGCATCTACAGGACCCGCTGAGCCTTGGCTGCGACACTAC 129
 QY 691 TTCTGGCGCGCTGCTGCTGAGGAGCTGGGTGGCGGAGAGGGCGGAGGGCGCCGCGAC 750
 Db 130 TTCTGGCGCGCTGCTGCTGAGGAGCTGGGTGGCGGAGAGGGCGGAGGGCGCCGCGAC 189
 QY 751 TGCCCGAGTGGCGGGCGACGTTGCGCGAGCCCGCTGGCGCCAGCCTCAAGCTGGCC 810
 Db 190 TGCCCGAGTGGCGGGCGACGTTGCGCGAGCCCGCTGGCGCCAGCCTCAAGCTGGCC 249
 QY 811 AACATCGTGAGCGCTACAGCTCTTCCGCTGAGCGCCATCTCTCAACGGCGCGCGGCC 870
 Db 250 AACATCGTGAGCGCTACAGCTCTTCCGCTGAGCGCCATCTCTCAACGGCGCGCGGCC 309
 QY 871 GCGGACCTCCGAGGCGCAGCAAGGTCAAGCTCTTCTGCTCAGCGACCGCGCGCTT 930
 Db 310 GCGGACCTCCGAGGCGCAGCAAGGTCAAGCTCTTCTGCTCAGCGACCGCGCGCTT 369
 QY 931 CTCTGCTTCTTCTGCGAGCGCTGCTGCTGAGCGAGCATGAGTCAACGGCGCGCGGCC 990
 Db 370 CTCTGCTTCTTCTGCGAGCGCTGCTGCTGAGCGAGCATGAGTCAACGGCGCGGCC 429
 QY 991 GAGCCTTCGACGAGCTGCGAGGAGCTGAAGACCACTTCAAGGCGCTTCAAGACAGC 1050
 Db 430 GAGCCTTCGACGAGCTGCGAGGAGCTGAAGACCACTTCAAGGCGCTTCAAGACAGC 489
 QY 1051 GAGCGGAAACACACCGAGCGCTGCTGCTGAGCGCAACTGCGGAGGAGCAAGTCT 1110
 Db 490 GAGCGGAAACACACCGAGCGCTGCTGCTGAGCGCAACTGCGGAGGAGCAAGTCT 549
 QY 1111 TCACCAAGAGCTGCGGACCACTATCGCGAGCGCTTCTGAGCGGCTGCAACCGGCTGCTG 1170
 Db 550 TCACCAAGAGCTGCGGACCACTATCGCGAGCGCTTCTGAGCGGCTGCAACCGGCTGCTG 609
 QY 1171 CGTGAACCGCAGAGGCCATCTAGAGAGCTGAGGCGGACACGCGCCGCGACCTGACC 1230
 Db 610 CGTGAACCGCAGAGGCCATCTAGAGAGCTGAGGCGGACACGCGCCGCGACCTGACC 669
 QY 1231 GACATCGAGCAGAAAGTCCAGCGCTACAGCGAGCTGCGGCAAGGTCAGGAGGAGCC 1290
 Db 670 GACATCGAGCAGAAAGTCCAGCGCTACAGCGAGCTGCGGCAAGGTCAGGAGGAGCC 729
 QY 1291 CAGATCTCGAGGAGCGGCTGGTGAACCGACCGCGCACACTTCTCTGGCTGGGCTGGCC 1350
 Db 730 CAGATCTCGAGGAGCGGCTGGTGAACCGACCGCGCACACTTCTCTGGCTGGGCTGGCC 789
 QY 1351 TCACTGTCGAGCGGCTCAAGGGAAAAATCCATGAGACCACTCAATATGAAGACTTC 1410
 Db 790 TCACTGTCGAGCGGCTCAAGGGAAAAATCCATGAGACCACTCAATATGAAGACTTC 849
 QY 1411 CCGACCTCCAGTACAGGCGCCCTGCTGCTGAGTACCACTCTGGAAGTCCCTGTTCCAGGAC 1470
 Db 850 CCGACCTCCAGTACAGGCGCCCTGCTGCTGAGTACCACTCTGGAAGTCCCTGTTCCAGGAC 909
 QY 1471 ATCCACCCAGTGGCGCGGCTTAACCTGGAGCCCGGGGACAGCCCAAGCGGCTGATC 1530
 Db 910 ATCCACCCAGTGGCGCGGCTTAACCTGGAGCCCGGGGACAGCCCAAGCGGCTGATC 969
 QY 1531 CTGTGCGACGACTGCACCATTTGGCTTACGGCACTTGCACCCACAGCCACTTCAGGAC 1590
 Db 970 CTGTGCGACGACTGCACCATTTGGCTTACGGCACTTGCACCCACAGCCACTTCAGGAC 1029
 QY 1591 TCGCCAAAGCGCTTCGATGTTGGAGTGTGCGTGTGCGTGTCTGAAAGCTTCAGTAGTGGC 1650
 Db 1030 TCGCCAAAGCGCTTCGATGTTGGAGTGTGCGTGTGCGTGTCTGAAAGCTTCAGTAGTGGC 1089

Qy		1651	GTCACCTACTGGGAGGTGGTGGCCGGAGAAGACCAGTTGGGTGATCGGGCTGGCACAC	1710
Db		1090	GTCACCTACTGGGAGGTGGTGGCCGGAGAAGACCAGTTGGGTGATCGGGCTGGCACAC	1149
Qy		1711	GAAGCCGAAGCCGCAAGGCNGCATCCAGATCCAGGCCAGCCGCGGCTTCTACTGCATC	1770
Db		1150	GAAGCCGAAGCCGCAAGGCAGCATCCAGATCCAGCCCAGCCGCGGCTTCTACTGCATC	1209
Qy		1771	GTGATGCAGATGGCAAACCAAGTACAGCGCCTGCACGGAGCCCTGGACCGCGCTTAACGTC	1830
Db		1210	GTGATGCAGATGGCAAACCAAGTACAGCGCCTGCACGGAGCCCTGGACCGCGCTTAACGTC	1269
Qy		1831	CGGGAAGAAGCTTGACAAGGTGGGTGTTCTCTGGACTATGACCAAGGCTTGCTCATCTTC	1890
Db		1270	CGGGAAGAAGCTTGACAAGGTGGGTGTTCTCTGGACTATGACCAAGGCTTGCTCATCTTC	1329
Qy		1891	TACAACTGCTGATGACATGTCCTGCTCTACACCTTCGCGAGAAGTTCCCTGGCAAGCTC	1950
Db		1330	TACAACTGCTGATGACATGTCCTGCTCTACACCTTCGCGAGAAGTTCCCTGGCAAGCTC	1389
Qy		1951	TGCTCTTACTTCAGCCCTGGCCAGAGCCACGCCAATGGCAAGAACGTTAGCCGCTCGG	2010
Db		1390	TGCTCTTACTTCAGCCCTGGCCAGAGCCACGCCAATGGCAAGAACGTTAGCCGCTCGG	1449
Qy		2011	ATCAACACCGTCCGCATCTAGTCCAGGCAGAAGAGACCAACCTCTCTGGHACCACTGC	2070
Db		1450	ATCAACACCGTCCGCATCTAGTCCAGGCAGAAGAGAGACCAACCTCTCTGGHACCACTGC	1509
Qy		2071	CACCTGCAAGAGCCCTCCCAAGGAAGATAGAAGACCTGGACTCCAGCCCCACCGTGGCCAC	2130
Db		1510	CACCTGCAAGAGCCCTCCCAAGGAAGATAGAAGACCTGGACTCCAGCCCCACCGTGGCCAC	1568
Qy		2131	TGGAGACCTCAGGCCAGTTGTTTACCTCCAGCCTCCAGTCTGTATAAATGGAGTTGTCAT	2190
Db		1569	TGGAGACCTCAGGCCAGTTGTTTACCTCCAGCCTCCAGTCTGTATAAATGGAGTTGTCAT	1628
Qy		2191	TCCTACTCTCTAAACHCTCTCCAGCATCGATGTTCTGTAGTCTTGACCTGTATTAGGGA	2250
Db		1629	TCCTACTCTCTAAACHCTCTCCAGCATCGATGTTCTGTAGTCTTGACCTGTATTAGGGA	1688
Qy		2251	TACAGCTTTGATCCAAGGATGTACATGGCTTCTCCTCAGGGCAACCCCTGCCCAACCCCT	2310
Db		1689	TACAGCTTTGATCCAAGGATGTACATGGCTTCTCCTCAGGGCAACCCCTGCCCAACCCCT	1748
Qy		2311	CATCCCACATCTTCCAGGGGAGGGGACTACCTTCCAGTGTCTCCCTCCAGGCCAGCCCT	2370
Db		1749	CATCCCACATCTTCCAGGGGAGGGGACTACCTTCCAGTGTCTCCCTCCAGGCCAGCCCT	1808
Qy		2371	GACCTCAGGAAGTGTACAGCATGGCCAGTAGTTGGCAGCCCGGAAGACACACAGCACCC	2430
Db		1809	GACCTCAGGAAGTGTACAGCATGGCCAGTAGTTGGCAGCCCGGAAGACACACAGCAC-CC	1867
Qy		2431	TCTTATGTCCCATGGCCTAAGACTTACCCCTGACCAAGCTAGTAGTGGGCCATTAGCCCT	2490
Db		1868	TCTTATGTCCCATGGCCTAAGACTTACCCCTGACCAAGCTAGTAGTGGGCCATTAGCCCT	1927
Qy		2491	TGACCCAGTCCACAGTGGTTCACAGGTAGTACCTGTGCTTAGGGTTGCCTGAGAGCCAAC	2550
Db		1928	TGACCCAGTCCACAGTGGTTCACAGGTAGTACCTGTGCTTAGGGTTGCCTGAGAGCCAAC	1987
Qy		2551	CTCTCTGCGCACCCCAACCAAGAACTATATGGTTCTACTTCTCCCACTGATCTGCTG	2610
Db		1988	CTCTCTGCGCACCCCAACCAAGAACTATATGGTTCTACTTCTCCCACTGATCTGCTG	2047
Qy		2611	GTCAAGTATGATGCTGTGGCCTGTGGGAAGGCACCTGGTAGTTGAGTCCACACATTTAGT	2670
Db		2048	GTCAAGTATGATGCTGTGGCCTGTGGGAAGGCACCTGGTAGTTGAGTCCACACATTTAGT	2107
Qy		2671	CATGTGCCACCACTTCTCTGCCCAACAGCCCGAGGGAAGGGTGAGGTATACCCAAAGCT	2730
Db		2108	CATGTGCCACCACTTCTCTGCCCAACAGCCCGAGGGAAGGGTGAGGTATACCCAAAGCT	2167

QY	2731	GATCGAGAGCCATTAGCCTAAAGAACTGTCAGGACAAGCCTCCCTGGATGATCGAGGT	2790
DB	2168	GATCGAGAGCCATTATAGCCTAAAGAACTGTCAGGACAAGCCTCCCTGGATGATCGAGGT	2227
QY	2791	CCCAGTAGCTCTCAACAAGAGTCCAGCAACCTCTTTACGCAAGGCTCTGTCACTGC	2850
DB	2228	CCCAGTAGCTCTGAAACAAGTCCAGCAACCTCTTTACGCAAGGCTCTGTGACCTGC	2287
QY	2851	TAGGGTGCAGGAGCTTCCAGAAAGCAGTTGTTGTAATTAGCAACCAAGCACTGGAGGGG	2910
DB	2288	TAGGGTGCAGGAGCTTCCAGAAAGCAGTTGTTGTAATTAGCAACCAAGCACTGGAGGGG	2347
QY	2911	CTGTTGCTAGACCCCTGTTCAGACTTGGCACTTATCTCACTTAGGATCTCTGCTGCAGAA	2970
DB	2348	CTGTTGCTAGACCCCTGTTCAGACTTGGCACTTATCTCACTTAGGATCTCTGCTGCAGAA	2407
QY	2971	AACAAGAGCCACTTGTAGCTGGTTTAATTAGACAAGGATTTACTACTGGCCCTCGTGG	3030
DB	2408	AACAAGAGCCACTTGTAGCTGGTTTAATTAGACAAGGATTTACTACTGGCCCTCGTGG	2467
QY	3031	CTTGCAAAATGTTGGAAGAGCTGGAGAAGCAGACTCTGCTGTAATTTCCAGGAACCTCCCA	3090
DB	2468	CTTGCAAAATGTTGGAAGAGCTGGAGAAGCAGACTCTGCTGTAATTTCCAGGAACCTCCCA	2527
QY	3091	CGCGCAGATTCACTCATGCTCTGTTGTGTGACAGGAAGCTGCCCCCATCTGCAGGAAGCCAC	3150
DB	2528	CGCGCAGATTCACTCATGCTCTGTTGTGTGACAGGAAGCTGCCCCCATCTGCAGGAAGCCAC	2587
QY	3151	TATGCCAGAAAGCTGTGACTGCAGAACTAGGCTCCCTCTTGCCAAGTCCGTCAGGCCA	3210
DB	2588	TATGCCAGAAAGCTGTGACTGCAGAACTAGGCTCCCTCTTGCCAAGTCCGTCAGGCCA	2647
QY	3211	ATAGATGTCCTGGGCTGCCCTCTCCCACTTCACCTCAGTTCCTCCAAATCTAAATTTTAA	3270
DB	2648	ATAGATGTCCTGGGCTGCCCTCTCCCACTTCACCTCAGTTCCTCCAAATCTAAATTTTAA	2707
QY	3271	CAAGAGATTCTGTTTGGGGAACTTAAGTCAGATCCAGAACTTTGGCTGCAAGGGAGTCT	3330
DB	2708	CAAGAGATTCTGTTTGGGGAACTTAAGTCAGATCCAGAACTTTGGCTGCAAGGGAGTCT	2767
QY	3331	GGGAAATGTCATTTCCCTAGAAGAACTTAGGTTAGGTTGGTGGAGCAGCCCCACCTGCCGTTT	3390
DB	2768	GGGAAATGTCATTTCCCTAGAAGAACTTAGGTTAGGTTGGTGGAGCAGCCCCACCTGCCGTTT	2827
QY	3391	TTCTGCCACAGCATCCAACTCGTGAAGAACTCGGAGAGGGTGGAGTCCACATCTTAGGGTT	3450
DB	2828	TTCTGCCACAGCATCCAACTCGTGAAGAACTCGGAGAGGGTGGAGTCCACATCTTAGGGTT	2887
QY	3451	GTCCTGCCCTTTGGCTCTATCCCTGCCAGAGTGGGAACTGGAGGAGTGGGCTGCAAGA	3510
DB	2888	GTCCTGCCCTTTGGCTCTATCCCTGCCAGAGTGGGAACTGGAGGAGTGGGCTGCAAGA	2947
QY	3511	CTGAGCCTAAATGTCCTCCCGGCTTCACATTTCTTTCTAGTCTCGGGGCTTAGATTCTG	3570
DB	2948	CTGAGCCTAAATGTCCTCCCGGCTTCACATTTCTTTCTAGTCTCGGGGCTTAGATTCTG	3007
QY	3571	CACTTGGGGTCTTGACACAAACACCATCCCAAAGTAGCGGAAGAGCTAAACACAGGG	3630
DB	3008	CACTTGGGGTCTTGACACAAACACCATCCCAAAGTAGCGGAAGAGCTAAACACAGGG	3067
QY	3631	GGTTCTTAAATGGCTGCCCGGCCACCCGGGCTCCCTTGGGCAAAAGAAATGTGCAGC	3690
DB	3068	GGTTCTTAAATGGCTGCCCGGCCACCCGGGCTCCCTTGGGCAAAAGAAATGTGCAGC	3127
QY	3691	CCTACCCCAACCCCTTCAACTACCAAGATCTGGGCGCACCCCGCAGATTTTTATTAAAAA	3750
DB	3128	CCTACCCCAACCCCTTCAACTACCAAGATCTGGGCGCACCCCGCAGATTTTTATTAAAAA	3187
QY	3751	TGTTGCCCATTTATGAGTTATGATCAATTTGTAATAAATAAGTTACAGATGTC	3806
DB	3188	TGTTGCCCATTTATGAGTTATGATCAATTTGTAATAAATAAGTTACAGATGTC	3243

```

RESULT 4
ID ABX76356 standard; DNA; 4702 BP.
XX
AC ABX76356;
XX
DT 02-APR-2003 (first entry)
XX
DE Lung cancer-associated polynucleotide #220.
XX
KW Lung cancer-associated polynucleotide; gene; ds; cytostatic; emphysema;
KW antiinflammatory; antiasthmatic; non-small cell lung cancer; atelectasis;
KW small cell lung cancer; benign lesion; precancerous lesion; bronchitis;
KW chronic obstructive pulmonary disease; hypersensitivity pneumonitis;
KW interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.
XX
OS Unidentified.
XX
PN WO200286443-A2.
XX
PD 31-OCT-2002.
XX
PF 18-APR-2002; 2002WO-US012476.
XX
PR 18-APR-2001; 2001US-0284770P.
PR 10-MAY-2001; 2001US-0290492P.
PR 09-NOV-2001; 2001US-0339245P.
PR 13-NOV-2001; 2001US-0350666P.
PR 23-NOV-2001; 2001US-0334370P.
PR 12-APR-2002; 2002US-0372246P.
XX
PA (BOCB-) EOS BIOTECHNOLOGY INC.
XX
PI Aziz N, Murray R;
XX
DR WPI; 2003-093161/08.
DR P-PSDB; ABUS6627.
XX
PT Detecting a lung cancer-associated transcript in a cell from a patient
PT for treating lung cancer, by contacting a biological sample from the
PT patient with a polynucleotide that exhibits increased or decreased
PT expression in lung cancer.
XX
PS Claim 22; Page 355-356; 453pp; English.
XX
CC The invention relates to a method for detecting a lung cancer-associated
CC transcript in a cell from a patient, comprising contacting a biological
CC sample from the patient with a polynucleotide that selectively hybridises
CC to a sequence that is at least 80 % identical to a gene that exhibits
CC increased or decreased expression in lung cancer samples. Lung cancer-
CC associated polynucleotides and polypeptides are used for identifying a
CC compound that modulates a lung cancer-associated polypeptide, for
CC inhibiting proliferation of a lung cancer-associated cell to treat lung
CC cancer in a patient and for treating a mammal having lung cancer by
CC administering a modulatory compound identified. The methods are useful
CC for treating lung cancer, such as small cell lung cancer, non-small cell
CC lung cancer or other benign or precancerous lesions, e.g. atelectasis,
CC emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis,
CC hypersensitivity pneumonitis, interstitial pulmonary fibrosis, asthma and
CC bronchiectasis. The genes, polynucleotides and polypeptides are useful
CC for diagnostic purposes and as targets for screening for therapeutic
CC compounds that modulate lung cancer, such as antibodies. Sequences
CC ABX76124-ABX76474 represent lung cancer-associated polynucleotides of the
CC invention
XX
SQ Sequence 4702 BP; 1159 A; 1218 C; 1217 G; 1108 T; 0 U; 0 Other;
Query Match 0.7%; Score 26; DB 7; Length 4702;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3801 GATGTCACAAAAA 3826
|||||
ID ABQ92018 standard; cDNA; 2522 BP.
XX
RESULT 6
ID ABQ92018
XX
DB 2495 ATGTCACAAAAA 2519
|||||
QY 3802 ATGTCACAAAAA 3826
|||||
Query Match 0.7%; Score 25; DB 2; Length 2522;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3802 ATGTCACAAAAA 3826
|||||
DB 2495 ATGTCACAAAAA 2519
|||||
QY 3801 GATGTCACAAAAA 3826
|||||
ID ABQ92018 standard; cDNA; 2522 BP.
XX

```

Db 4660 GATGTCACAAAAA 4685

RESULT 5

AAV82781

ID AAV82781 standard; cDNA; 2522 BP.

XX

AC AAV82781;

XX

DT 25-FEB-1999 (first entry)

XX

DE Clone df396_1 isolated from human adult brain cDNA library.

XX

KW Secreted protein; nutritional activity; immune stimulating; vaccine;

KW suppressing activity; haematopoiesis regulating activity;

KW tissue growth activity; activin; inhibin activity; chemotaxis;

KW chemokinetic activity; haemostasis; thrombolytic activity; receptor;

KW ligand; anti-inflammatory; cadherin; tumour invasion suppressor;

KW tumour inhibition; gene therapy; ds.

XX

OS Homo sapiens.

XX

PN WO9842739-A2.

XX

PD 01-OCT-1998.

XX

PF 20-MAR-1998; 98WO-US005653.

XX

PR 21-MAR-1997; 97US-00822167.

PR 19-MAR-1998; 98US-00044466.

XX

PA (GEMY) GENETICS INST INC.

XX

PI Jacobs K, McCoy JM, Lavallie ER, Racie LA, Merberg D, Treacy M;

PI Spaulding V, Agostino MJ;

XX

DR WPI; 1998-609890/51.

DR P-PSDB; AAW85458.

XX

PT New polynucleotides encoding secreted human proteins - derived from human

PT foetal brain, adult brain, foetal kidney, placenta or adult pineal gland

PT cDNA libraries.

XX

PS Claim 20; Page 74-76; 113pp; English.

XX

CC The present sequence encodes a secreted protein. The polynucleotide and

CC secreted protein are predicted to have biological activities which would

CC make them suitable for treating, preventing or ameliorating medical

CC conditions in humans and animals, although no supporting data is given.

CC Suggested activities include nutritional activity, immune stimulating

CC (e.g. as vaccines) or suppressing activity, haematopoiesis regulating

CC activity, tissue growth activity, activin/inhibin activity,

CC chemotactic/chemokinetic activity, haemostatic and thrombolytic activity,

CC receptor/ligand activity, anti-inflammatory activity, cadherin/tumour

CC invasion suppressor activity, and tumour inhibition activity (no data is

CC given in the specification to support these activities). The

CC polynucleotide is also stated to be useful for gene therapy

XX

SQ Sequence 2522 BP; 558 A; 683 C; 608 G; 673 T; 0 U; 0 Other;

Query Match 0.7%; Score 25; DB 2; Length 2522;

Best Local Similarity 100.0%; Pred. No. 28;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3802 ATGTCACAAAAA 3826

|||||

DB 2495 ATGTCACAAAAA 2519

|||||

RESULT 6

ABQ92018

ID ABQ92018 standard; cDNA; 2522 BP.

XX

SQ Sequence 2647 BP; 942 A; 475 C; 384 G; 837 T; 0 U; 9 Other;

Query Match 0.7%; Score 25; DB 5; Length 2647;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3802 ATGTCAAAAAAAAAAAAAAAAAAAAA 3826
|||||
Db 58 ATGTCAAAAAAAAAAAAAAAAAAAAA 34

RESULT 10

ABV25449/c
ID ABV25449 standard; cDNA; 2647 BP.

AC ABV25449;

DT 16-SEP-2002 (first entry)

XX Human prostate expression marker cDNA 25440.

XX Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
KW pharmacogenomic marker; gene; ss.

OS Homo sapiens.

XX WO200160860-A2.

PN 23-AUG-2001.

PD 20-FEB-2001; 2001WO-US005171.

PR 17-FEB-2000; 2000US-0183319P.

PR 16-MAR-2000; 2000US-0189862P.

PR 25-MAY-2000; 2000US-0207454P.

PR 09-JUN-2000; 2000US-0211314P.

PR 19-JUL-2000; 2000US-0219007P.

PR 13-DEC-2000; 2000US-0255281P.

XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

XX Schlegel R, Endege WO, Monahan JE;

PI WPI; 2001-662795/76.

XX Novel isolated nucleic acid molecule associated with cancerous state of

PT prostate cells and correlating with presence of prostate cancer, useful

PT for detecting presence of prostate cancer, stage of prostate cancer.

XX Claim 1; Page 5047-5048; 11750pp; English.

XX The invention relates to an isolated nucleic acid molecule (I) comprising

CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the

CC specification or its complement. (I) is useful for: (a) assessing whether

CC a patient is afflicted with prostate cancer; (b) monitoring the

CC progression of prostate cancer in a patient; (c) assessing the efficacy

CC of a test compound to inhibit prostate cancer in a patient; (d) assessing

CC the efficacy of a therapy for inhibiting prostate cancer in a patient;

CC (e) selecting a composition for inhibiting prostate cancer in a patient;

CC (f) assessing the prostate cell carcinogenic potential of a compound; (g)

CC determining whether prostate cancer has metastasized in a patient; (h)

CC assessing the aggressiveness or indolence of prostate cancer in a patient

CC ; (I) is also useful as a pharmacodynamic or pharmacogenomic marker

XX Sequence 2647 BP; 942 A; 475 C; 384 G; 837 T; 0 U; 9 Other;

SQ Query Match 0.7%; Score 25; DB 5; Length 2647;

Best Local Similarity 100.0%; Pred. No. 28;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3802 ATGTCAAAAAAAAAAAAAAAAAAAAA 3826

|||||

Db 58 ATGTCAAAAAAAAAAAAAAAAAAAAA 34

RESULT 11

ABV30164/c

ID ABV30164 standard; cDNA; 2647 BP.

XX AC ABV30164;

XX 16-SEP-2002 (first entry)

XX Human prostate expression marker cDNA 30155.

XX Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
KW pharmacogenomic marker; gene; ss.

OS Homo sapiens.

XX WO200160860-A2.

PN 23-AUG-2001.

PD 20-FEB-2001; 2001WO-US005171.

PR 17-FEB-2000; 2000US-0183319P.

PR 16-MAR-2000; 2000US-0189862P.

PR 25-MAY-2000; 2000US-0207454P.

PR 09-JUN-2000; 2000US-0211314P.

PR 18-JUL-2000; 2000US-0219007P.

PR 13-DEC-2000; 2000US-0255281P.

XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

XX Schlegel R, Endege WO, Monahan JE;

PI WPI; 2001-662795/76.

XX Novel isolated nucleic acid molecule associated with cancerous state of

PT prostate cells and correlating with presence of prostate cancer, useful

PT for detecting presence of prostate cancer, stage of prostate cancer.

XX Claim 1; Page 6531; 11750pp; English.

XX The invention relates to an isolated nucleic acid molecule (I) comprising

CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the

CC specification or its complement. (I) is useful for: (a) assessing whether

CC a patient is afflicted with prostate cancer; (b) monitoring the

CC progression of prostate cancer in a patient; (c) assessing the efficacy

CC of a test compound to inhibit prostate cancer in a patient; (d) assessing

CC the efficacy of a therapy for inhibiting prostate cancer in a patient;

CC (e) selecting a composition for inhibiting prostate cancer in a patient;

CC (f) assessing the prostate cell carcinogenic potential of a compound; (g)

CC determining whether prostate cancer has metastasized in a patient; (h)

CC assessing the aggressiveness or indolence of prostate cancer in a patient

CC ; (I) is also useful as a pharmacodynamic or pharmacogenomic marker

XX Sequence 2647 BP; 942 A; 475 C; 384 G; 837 T; 0 U; 9 Other;

SQ Query Match 0.7%; Score 25; DB 5; Length 2647;

Best Local Similarity 100.0%; Pred. No. 28;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3802 ATGTCAAAAAAAAAAAAAAAAAAAAA 3826

|||||

Db 58 ATGTCAAAAAAAAAAAAAAAAAAAAA 34

RESULT 12

ABV25571/c

ID ABV25571 standard; cDNA; 2647 BP.

XX AC ABV25571;

XX 16-SEP-2002 (first entry)

```

XX DE Human prostate expression marker cDNA 25562.
XX KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
XX KW pharmacogenomic marker; gene; ss.
XX OS Homo sapiens.
XX PN WO200160860-A2.
XX PD 23-AUG-2001.
XX PF 20-FEB-2001; 2001WO-US005171.
XX PI 17-FEB-2000; 2000US-0183319P.
XX PR 16-MAR-2000; 2000US-0189862P.
XX PR 25-MAY-2000; 2000US-0207454P.
XX PR 09-JUN-2000; 2000US-0211314P.
XX PR 18-JUL-2000; 2000US-0219007P.
XX PR 13-DEC-2000; 2000US-0255281P.
XX PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX PI Schlegel R, Endege WO, Monahan JE;
XX WI; 2001-662795/76.
XX PT Novel isolated nucleic acid molecule associated with cancerous state of
XX PT prostate cells and correlating with presence of prostate cancer, useful
XX PT for detecting presence of prostate cancer, stage of prostate cancer.
XX PS Claim 1; Page 5100; 11750pp; English.
XX CC The invention relates to an isolated nucleic acid molecule (I) comprising
XX CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
XX CC specification or its complement. (I) is useful for: (a) assessing whether
XX CC a patient is afflicted with prostate cancer; (b) monitoring the
XX CC progression of prostate cancer in a patient; (c) assessing the efficacy
XX CC of a test compound to inhibit prostate cancer in a patient; (d) assessing
XX CC the efficacy of a therapy for inhibiting prostate cancer in a patient;
XX CC (e) selecting a composition for inhibiting prostate cancer in a patient;
XX CC (f) assessing whether prostate cancer has metastasized in a patient; (g)
XX CC determining whether prostate cancer has metastasized in a patient; (h)
XX CC assessing the aggressiveness or indolence of prostate cancer in a patient
XX CC ; (I) is also useful as a pharmacodynamic or pharmacogenomic marker
XX SQ Sequence 2647 BP; 942 A; 475 C; 384 G; 837 T; 0 U; 9 Other;

Query Match 0.7%; Score 25; DB 5; Length 2647;
Best Local Similarity 100.0%; Pred.No. 28;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3802 ATGTCAAAAA...AAAAAAAAA 3826
DB 58 ATGTCAAAAA...AAAAAAAAA 34

RESULT 13
ABV29143/c
ID ABV29143 standard; cDNA; 2647 BP.
XX AC ABV29143;
XX DT 16-SEP-2002 (first entry)
XX DE Human prostate expression marker cDNA 29134.
XX KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
XX KW pharmacogenomic marker; gene; ss.
XX OS Homo sapiens.
XX PN WO200160860-A2.

Human prostate expression marker cDNA 25562.
Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
pharmacogenomic marker; gene; ss.
Homo sapiens.
WO200160860-A2.
23-AUG-2001.
20-FEB-2001; 2001WO-US005171.
17-FEB-2000; 2000US-0183319P.
16-MAR-2000; 2000US-0189862P.
25-MAY-2000; 2000US-0207454P.
09-JUN-2000; 2000US-0211314P.
18-JUL-2000; 2000US-0219007P.
13-DEC-2000; 2000US-0255281P.
(MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Schlegel R, Endege WO, Monahan JE;
WI; 2001-662795/76.
Novel isolated nucleic acid molecule associated with cancerous state of
prostate cells and correlating with presence of prostate cancer, useful
for detecting presence of prostate cancer, stage of prostate cancer.
Claim 1; Page 5100; 11750pp; English.
The invention relates to an isolated nucleic acid molecule (I) comprising
a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
specification or its complement. (I) is useful for: (a) assessing whether
a patient is afflicted with prostate cancer; (b) monitoring the
progression of prostate cancer in a patient; (c) assessing the efficacy
of a test compound to inhibit prostate cancer in a patient; (d) assessing
the efficacy of a therapy for inhibiting prostate cancer in a patient;
(e) selecting a composition for inhibiting prostate cancer in a patient;
(f) assessing whether prostate cancer has metastasized in a patient; (g)
determining whether prostate cancer has metastasized in a patient; (h)
assessing the aggressiveness or indolence of prostate cancer in a patient
; (I) is also useful as a pharmacodynamic or pharmacogenomic marker
Sequence 2647 BP; 942 A; 475 C; 384 G; 837 T; 0 U; 9 Other;

Query Match 0.7%; Score 25; DB 5; Length 2647;
Best Local Similarity 100.0%; Pred.No. 28;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3802 ATGTCAAAAA...AAAAAAAAA 3826
DB 58 ATGTCAAAAA...AAAAAAAAA 34

RESULT 14
AAV35727
ID AAV35727 standard; cDNA; 2796 BP.
XX AC AAV35727;
XX DT 09-JUL-1999 (first entry)
XX DE cDNA encoding a protein identified by the signal sequence trap method.
XX KW Signal sequence trap method; SST method; immunisation; inhibition;
XX KW infection; allergy; cancer; regulation; tissue formation; tissue repair;
XX KW activin activity; inhibin activity; chemokine activity;
XX KW cytokine activity; blood coagulation regulation; agonist; antagonist;
XX KW metabolic disorder; hormonal disorder; immune disorder;
XX KW severe combined immunodeficiency; SCID; AIDS; thrombosis; cancer; wound;
XX KW ss.
XX OS Homo sapiens.
XX PN WO9918126-A1.
XX PD 15-APR-1999.
XX PF 06-OCT-1998; 98WO-JP004514.

```

```
XX 07-OCT-1997; 97JP-00274674.
XX (ONCY ) ONO PHARM CO LTD.
XX
XX Fukushima D, Shibayama S, Tada H;
XX WPI; 1999-277254/23.
XX DR P-PSDB; AAY02374.
XX
XX Polypeptides identified by the signal sequence trap method from a human
XX cDNA library.
XX
XX Claim 4; Page 153-157; 281pp; Japanese.
XX
XX AAX35694-X35747 represent cDNA sequences that encode novel polypeptides
XX (AAY02358-84) which are identified from a human placental cDNA library by
XX the signal sequence trap (SST) method. The polypeptides have a broad
XX range of physiological activity, including immunisation against and
XX inhibition of infectious, allergies and cancer; regulation of tissue
XX formation and repair; activin/inhibin activity; chemokine/cytokine
XX activity; blood coagulation regulation; and receptor/ligand agonist or
XX antagonist activity. The polypeptides can be used for prevention and
XX treatment of disorders including infections by bacteria, yeasts and
XX viruses (including HIV) and protozoa; metabolic and hormonal disorders;
XX immune disorders (including severe combined immunodeficiency (SCID) and
XX AIDS; thrombosis; cancer; and traumatic or surgical wounds
XX
XX Sequence 2796 BP; 636 A; 690 C; 674 G; 796 T; 0 U; 0 Other;
XX
XX Query Match 0.7%; Score 25; DB 2; Length 2796;
XX Best Local Similarity 100.0%; Pred. No. 28;
XX Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 3802 ATGTCAAAAAAAAAAAAAAAAAAAAA 3826
XX Db |||||
XX 2768 ATGTCAAAAAAAAAAAAAAAAAAAAA 2792
XX
XX RESULT 15
XX ADD69641
XX ID ADD69641 standard; cDNA; 3858 BP.
XX AC
XX ADD69641;
XX
XX 15-JAN-2004 (first entry)
XX
XX Human REMAP cDNA - SEQ ID 70.
XX
XX human; receptor and membrane-associated protein; REMAP; cytoskeletal;
XX antiarteriosclerotic; anticonvulsant; neurotropic; neuroprotective;
XX cerebrotective; anti-HIV; anti-allergic; anti-inflammatory;
XX thymomimetic; cell proliferative; cancer; atherosclerosis; neurological;
XX epilepsy; Huntington's disease; stroke; immune; inflammatory; AIDS;
XX allergy; developmental; hypothyroidism; Cushing's syndrome; infection;
XX ss; gene.
XX
XX Homo sapiens.
XX OS
XX
XX WO2003048305-A2.
XX PN
XX
XX 12-JUN-2003.
XX PD
XX
XX 13-NOV-2002; 2002WO-US036759.
XX PF
XX
XX 13-NOV-2001; 2001US-0333097P.
XX PR
XX 15-NOV-2001; 2001US-0335274P.
XX PR
XX 14-DEC-2001; 2001US-0340542P.
XX PR
XX 18-DEC-2001; 2001US-0342166P.
XX PR
XX 11-JAN-2002; 2002US-0347580P.
XX PR
XX 14-JAN-2002; 2002US-0348687P.
XX PR
XX (INCY-) INCYTE GENOMICS INC.
XX PA
```

```
XX Duggan BM, Yang J, Gietzen KJ, Lee SY, Tang YT, Azimzai Y;
XX Chawla NK, Warren BA, Barroso I, Becha SD, Yue H, Lehr-Mason PM;
XX Thangavelu K, Lee S, Emerling BM, Kadle AE, Khare R, Baughn MR;
XX Gandhi AR, Tran UK, Richardson TW, Marquis JP, Lal PG, Forsythe IJ;
XX Lee EA, Swarnakar A, Kallick DA, Griffin JA, Elliott VS, Gorvad AE;
XX Hafalia AJA, Ison CH, Jin P, Jiang X, Jackson AA, Bhatia U;
XX Burrill JD, Blake JJ, Ho A, Zheng W, Gao J;
XX
XX WPI; 2003-513744/48.
XX DR P-PSDB; ADD69594.
XX
XX New human receptors and membrane-associated proteins (REMAP), useful for
XX diagnosing, treating and preventing diseases or conditions associated
XX with the aberrant REMAP expression e.g. cancer, AIDS, atherosclerosis, or
XX infections.
XX
XX Claim 5; SEQ ID NO 70; 298pp; English.
XX
XX The invention relates to a novel isolated polypeptide comprising a human
XX receptor and membrane-associated protein (REMAP). The polypeptide of the
XX invention demonstrates cytostatic, antiarteriosclerotic, anticonvulsant,
XX neurotropic, neuroprotective, cerebrotective, anti-HIV, anti-allergic,
XX anti-inflammatory and thymomimetic activities and may be useful for
XX treating and diagnosing various disorders including those which are cell
XX proliferative such as cancer and atherosclerosis, neurological including
XX epilepsy, Huntington's disease and stroke, immune/inflammatory
XX particularly AIDS and allergies and developmental such as hypothyroidism
XX and Cushing's syndrome, as well as infections. The current sequence is
XX that of the human REMAP cDNA of the invention.
XX
XX SQ Sequence 3858 BP; 972 A; 961 C; 989 G; 936 T; 0 U; 0 Other;
XX
XX Query Match 0.7%; Score 25; DB 9; Length 3858;
XX Best Local Similarity 100.0%; Pred. No. 26;
XX Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 3802 ATGTCAAAAAAAAAAAAAAAAAAAAA 3826
XX Db |||||
XX 3815 ATGTCAAAAAAAAAAAAAAAAAAAAA 3839
XX
XX Search completed: September 4, 2004, 08:48:49
XX Job time : 950 secs
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; OTHER INFORMATION: 99-27349-267.mis2
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1748..1767
; OTHER INFORMATION: upstream amplification primer, complement
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1337..1355
; OTHER INFORMATION: downstream amplification primer
; FEATURE:
; NAME/KEY: misc binding
; LOCATION: 1489..1513
; OTHER INFORMATION: 99-27349-267 probe
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 182,848,1501,2206,2397
; OTHER INFORMATION: n=a, g, c or t
US-09-539-333D-222
```

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Query Match          0.6%; Score 24; DB 4; Length 3001;
Best Local Similarity 100.0%; Pred. No. 0.92;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Qy 3803 TGTCAAAAAAAAAAAAAAAAAAAAAA 3826
      |||
Db 2367 TGTCAAAAAAAAAAAAAAAAAAAAAA 2390
```

RESULT 2

```
US-09-112-096-28
; Sequence 28, Application US/09112096
; Patent No. 6194152
; GENERAL INFORMATION:
; APPLICANT: Reiner Laus
; APPLICANT: Michael H. Shaperro
; APPLICANT: Larisa Tsavaler
; TITLE OF INVENTION: Prostate Tumor Polynucleotide and
; TITLE OF INVENTION: Antigen Compositions
; FILE REFERENCE: 7636-0015.30
; CURRENT APPLICATION NUMBER: US/09/112,096
; CURRENT FILING DATE: 1998-07-09
; EARLIER APPLICATION NUMBER: 60/056,110
; EARLIER FILING DATE: 1997-08-20
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 28
; LENGTH: 3848
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-112-096-28
```

```
Query Match          0.6%; Score 24; DB 3; Length 3848;
Best Local Similarity 100.0%; Pred. No. 0.91;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Qy 3803 TGTCAAAAAAAAAAAAAAAAAAAAAA 3826
      |||
Db 3780 TGTCAAAAAAAAAAAAAAAAAAAAAA 3803
```

RESULT 3

```
US-08-381-691-16/c
; Sequence 16, Application US/08381691
; Patent No. 5852224
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Alpha-lac Albumin Gene Constructs
; NUMBER OF SEQUENCES: 17
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
```

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/381,691
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3952 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-381-691-16
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```
Query Match          0.6%; Score 24; DB 2; Length 3952;
Best Local Similarity 100.0%; Pred. No. 0.91;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Qy 3803 TGTCAAAAAAAAAAAAAAAAAAAAAA 3826
      |||
Db 3856 TGTCAAAAAAAAAAAAAAAAAAAAAA 3833
```

RESULT 4

```
US-09-144-367-1
; Sequence 1, Application US/09144367
; Patent No. 6432639
; GENERAL INFORMATION:
; APPLICANT: Lichter, Jay
; APPLICANT: Guido, Marco
; TITLE OF INVENTION: GENOTYPING OF HUMAN CYP3A4
; FILE REFERENCE: SEQ-12P
; CURRENT APPLICATION NUMBER: US/09/144,367
; CURRENT FILING DATE: 1998-08-31
; PRIOR APPLICATION NUMBER: 60/058,612
; PRIOR FILING DATE: 1997-09-10
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 2759
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (70)...(1581)
; OTHER INFORMATION: Human CYP3A4 cDNA reference sequence
US-09-144-367-1
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Query Match          0.6%; Score 23; DB 4; Length 2759;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Qy 3804 GTCAAAAAAAAAAAAAAAAAAAAAA 3826
      |||
Db 2726 GTCAAAAAAAAAAAAAAAAAAAAAA 2748
```

RESULT 5

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US-09-705-299-10/c
; Sequence 10, Application US/09705299
; Patent No. 6440737
; GENERAL INFORMATION:
; APPLICANT: Lex M. Cowser
; APPLICANT: Susan M. Preier
; TITLE OF INVENTION: ANTISENSE MODULATION OF CELLULAR APOPTOSIS SUSCEPTIBILITY GENE
; FILE REFERENCE: RTS-0174
; CURRENT APPLICATION NUMBER: US/09/705,299
; CURRENT FILING DATE: 2000-11-01
; NUMBER OF SEQ ID NOS: 86
; SEQ ID NO 10
; LENGTH: 2929
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-705-299-10
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;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US94/10080
;; FILING DATE: HEREWITH
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/123,934
;; FILING DATE: 17-SEP-1993
;; CLASSIFICATION:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: LAZAR, Steven R
;; REGISTRATION NUMBER: 32,618
;; REFERENCE/DOCKET NUMBER: 5203-PCT
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (617) 498-8260
;; TELEFAX: (617) 876-5851
;; INFORMATION FOR SEQ ID NO: 5:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 3238 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
;; IMMEDIATE SOURCE:
;; CLONE: CFK1-10a
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: 474..2000
PCT-US94-10080-5

Query Match 0.6%; Score 23; DB 5; Length 3238;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3804 GTCACAAAAA...AAAAAAAAA 3826
|||...|||
DB 3157 GTCACAAAAA...AAAAAAAAA 3179

RESULT 9
US-09-688-188B-1
;; Sequence 1, Application US/09698188B
;; Patent No. 6656716
;; GENERAL INFORMATION:
;; APPLICANT: FLOWMAN, GREGORY
;; APPLICANT: MARTINEZ, RICARDO
;; APPLICANT: WHYTE, DAVID
;; TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES
;; FILE REFERENCE: 038602/0328
;; CURRENT APPLICATION NUMBER: US/09/688,188B
;; PRIOR FILING DATE: 2000-10-16
;; PRIOR APPLICATION NUMBER: 09/291,417
;; PRIOR FILING DATE: 1999-04-14
;; PRIOR APPLICATION NUMBER: 60/081,784
;; PRIOR FILING DATE: 1998-04-14
;; NUMBER OF SEQ ID NOS: 155
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 1
;; LENGTH: 3268
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-09-688-188B-1

Query Match 0.6%; Score 23; DB 4; Length 3268;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3804 GTCACAAAAA...AAAAAAAAA 3826
|||...|||
DB 3214 GTCACAAAAA...AAAAAAAAA 3236

RESULT 10

US-09-291-417D-1
;; Sequence 1, Application US/09291417D
;; Patent No. 6680170
;; GENERAL INFORMATION:
;; APPLICANT: FLOWMAN, GREGORY
;; APPLICANT: MARTINEZ, RICARDO
;; APPLICANT: WHYTE, DAVID
;; TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES
;; FILE REFERENCE: 038602/0329
;; CURRENT APPLICATION NUMBER: US/09/291,417D
;; CURRENT FILING DATE: 1999-04-13
;; PRIOR APPLICATION NUMBER: 60/081,784
;; PRIOR FILING DATE: 1998-04-14
;; NUMBER OF SEQ ID NOS: 155
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 1
;; LENGTH: 3268
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-09-291-417D-1

Query Match 0.6%; Score 23; DB 4; Length 3268;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3804 GTCACAAAAA...AAAAAAAAA 3826
|||...|||
DB 3214 GTCACAAAAA...AAAAAAAAA 3236

RESULT 11
US-09-336-643A-82
;; Sequence 82, Application US/09336643A
;; Patent No. 6399761
;; GENERAL INFORMATION:
;; APPLICANT: Miller, Andrew P.
;; APPLICANT: Curran, Mark Edward
;; APPLICANT: Hu, Ping
;; APPLICANT: Rutter, Marc
;; APPLICANT: Wang, Jian-Wang
;; TITLE OF INVENTION: No. 6399761el Human Potassium Channels
;; FILE REFERENCE: SEQ-15P
;; CURRENT APPLICATION NUMBER: US/09/336,643A
;; CURRENT FILING DATE: 1999-06-18
;; PRIOR APPLICATION NUMBER: 60/076,687
;; PRIOR FILING DATE: 1998-08-07
;; PRIOR APPLICATION NUMBER: 60/116,448
;; PRIOR FILING DATE: 1999-01-19
;; PRIOR APPLICATION NUMBER: PCT/US99/03826
;; PRIOR FILING DATE: 1999-02-22
;; NUMBER OF SEQ ID NOS: 87
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 82
;; LENGTH: 3300
;; TYPE: DNA
;; ORGANISM: H. sapiens
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: (50)...(1285)
US-09-336-643A-82

Query Match 0.6%; Score 23; DB 4; Length 3300;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3804 GTCACAAAAA...AAAAAAAAA 3826
|||...|||
DB 3242 GTCACAAAAA...AAAAAAAAA 3264

RESULT 12
US-09-819-989-1
;; Sequence 1, Application US/09819989

```
; Patent No. 6482629
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui et al.
; TITLE OF INVENTION: ISOLATED HUMAN ENZYME PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN ENZYME PROTEINS, AND USES
; FILE REFERENCE: THEREOF
; CURRENT APPLICATION NUMBER: CL001200
; CURRENT FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3377
; TYPE: DNA
; ORGANISM: Human
US-09-819-989-1

Query Match      0.6%; Score 23; DB 4; Length 3377;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3804 GTCACAAAAA 3826
Db 3339 GTCACAAAAA 3361

RESULT 13
US-10-273-992-1
; Sequence 1, Application US/10273992
; Patent No. 6664093
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui et al.
; TITLE OF INVENTION: ISOLATED HUMAN ENZYME PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN ENZYME PROTEINS, AND USES
; FILE REFERENCE: THEREOF
; CURRENT APPLICATION NUMBER: US/10/273,992
; CURRENT FILING DATE: 2002-10-21
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3377
; TYPE: DNA
; ORGANISM: Human
US-10-273-992-1

Query Match      0.6%; Score 23; DB 4; Length 3377;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3804 GTCACAAAAA 3826
Db 3339 GTCACAAAAA 3361

RESULT 14
US-09-866-028-6
; Sequence 6, Application US/09866028
; Patent No. 6642360
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerlitsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kijavini, Ivar
; APPLICANT: Napier, Mary
```

```
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/866,028
; CURRENT FILING DATE: 2001-05-25
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 6
; LENGTH: 3441
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-866-028-6

Query Match      0.6%; Score 23; DB 4; Length 3441;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3804 GTCACAAAAA 3826
Db 3406 GTCACAAAAA 3428

RESULT 15
US-09-083-351-1
; Sequence 1, Application US/09083351
; Patent No. 6087107
; GENERAL INFORMATION:
; APPLICANT: Sheffield, Val C.
; APPLICANT: Alward, Wallace L.M.
; APPLICANT: Stone, Edwin M.
; APPLICANT: Nishimura, Darryl
; APPLICANT: Patil, Shiva
; TITLE OF INVENTION: THERAPEUTICS AND DIAGNOSTICS FOR
; TITLE OF INVENTION: CONGENITAL HEART DISEASE BASED ON A NOVEL HUMAN
; TITLE OF INVENTION: TRANSCRIPTION FACTOR
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY, HOAG & ELIOT LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/083,351
; FILING DATE: 22-MAY-1998
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Arnold, Beth E.
; REGISTRATION NUMBER: 35,430
; REFERENCE/DOCKET NUMBER: UIA-029.02
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-832-1000
; TELEFAX: 617-832-7000
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3946 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 475..2133
US-09-083-351-1
```

Query Match 0.6%; Score 23; DB 3; Length 3946;
 Best Local Similarity 100.0%; Pred. No. 2.4;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3804 GTCACAAAAA 3826
 |||||
 Db 3919 GTCACAAAAA 3941

Search completed: September 4, 2004, 13:14:42
 Job time : 185 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 4, 2004, 08:32:53 ; Search time 1152 Seconds
(without alignments)
16508.391 Million cell updates/sec

Title: US-09-927-091-3

Perfect score: 3826

Sequence: 1 aggtcgctggaccgaagc.....aaaaaaaaaaaaaaaaa 3826

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 3267054 seqs, 2485319735 residues

Word size : 18

Total number of hits satisfying chosen parameters: 32167

Minimum DB seq length: 2500

Maximum DB seq length: 5000

Post-processing: Listing first 45 summaries

Database : Published Applications NA:*

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4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
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16: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
17: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
18: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
19: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3826	100.0	3826	9	US-09-927-091-3
2	26	0.7	4702	16	US-10-295-027-141
3	26	0.7	4702	16	US-10-295-027-1164
4	25	0.7	2511	17	US-10-437-963-100661
5	25	0.7	2522	9	US-09-745-763-39
6	25	0.7	2586	16	US-10-104-047-875
7	25	0.7	2629	15	US-10-106-698-1916
8	25	0.7	2796	9	US-09-529-063-51
9	25	0.7	2796	15	US-10-414-378-51
10	25	0.7	2806	13	US-10-424-599-137631
11	25	0.7	3465	17	US-10-615-659-11
12	25	0.7	3504	17	US-10-437-963-54840
13	25	0.7	3554	17	US-10-615-659-12
14	25	0.7	4572	17	US-10-450-826-108

15	25	0.7	4740	9	US-09-945-265-3	Sequence 3, Appli
16	25	0.7	4740	10	US-09-902-481A-2	Sequence 2, Appli
17	25	0.7	4740	15	US-10-207-655-175	Sequence 175, App
18	25	0.7	4740	15	US-10-136-819-18	Sequence 18, Appl
19	25	0.7	4740	16	US-10-159-563-339	Sequence 339, App
20	24	0.6	2509	9	US-09-925-301-540	Sequence 540, App
21	24	0.6	2602	17	US-10-437-963-11080	Sequence 11080, A
22	24	0.6	2633	9	US-09-764-877-2154	Sequence 2154, Ap
23	24	0.6	2633	16	US-10-242-515-2154	Sequence 2154, Ap
24	24	0.6	2645	14	US-10-044-090-799	Sequence 799, App
25	24	0.6	2661	16	US-10-159-563-399	Sequence 399, App
26	24	0.6	2661	17	US-10-211-179-4	Sequence 4, Appli
27	24	0.6	2677	10	US-09-733-643-1	Sequence 1, Appli
28	24	0.6	2840	9	US-09-978-295A-611	Sequence 611, App
29	24	0.6	2840	9	US-09-978-697-611	Sequence 611, App
30	24	0.6	2840	9	US-09-978-192A-611	Sequence 611, App
31	24	0.6	2840	9	US-09-999-832A-611	Sequence 611, App
32	24	0.6	2840	10	US-09-978-189-611	Sequence 611, App
33	24	0.6	2840	10	US-09-978-608A-611	Sequence 611, App
34	24	0.6	2840	10	US-09-978-585A-611	Sequence 611, App
35	24	0.6	2840	10	US-09-978-191A-611	Sequence 611, App
36	24	0.6	2840	10	US-09-978-403A-611	Sequence 611, App
37	24	0.6	2840	10	US-09-978-564A-611	Sequence 611, App
38	24	0.6	2840	10	US-09-999-833A-611	Sequence 611, App
39	24	0.6	2840	10	US-09-981-915A-611	Sequence 611, App
40	24	0.6	2840	10	US-09-978-824-611	Sequence 611, App
41	24	0.6	2840	10	US-09-918-585A-611	Sequence 611, App
42	24	0.6	2840	10	US-09-978-423A-611	Sequence 611, App
43	24	0.6	2840	10	US-09-978-193A-611	Sequence 611, App
44	24	0.6	2840	10	US-09-999-830A-611	Sequence 611, App
45	24	0.6	2840	10	US-09-978-757A-611	Sequence 611, App

ALIGNMENTS

RESULT 1

US-09-927-091-3
; Sequence 3, Application US/09927091
; Patent No. US20020119541A1
; GENERAL INFORMATION:
; APPLICANT: KILLARY, ANN
; APPLICANT: LOTT, STEVE
; APPLICANT: CHANDLER, DAWN
; TITLE OF INVENTION: THE TUMOR SUPPRESSOR CAR-1
; FILE REFERENCE: US06:651US
; CURRENT APPLICATION NUMBER: US/09/927,091
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 60/227,560
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: 60/225,033
; PRIOR FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 3826
; TYPE: DNA
; ORGANISM: Human
US-09-927-091-3

Query Match	100.0%;	Score 3826;	DB 9;	Length 3826;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 3826;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	AGCTCGCTGGACCGAAGCGGTGGCTGAAGCTCGCGGGGTAAGGGTCTCGCTGGG	60	
Db	1	AGCTCGCTGGACCGAAGCGGTGGCTGAAGCTCGCGGGGTAAGGGTCTCGCTGGG	60	
QY	61	CAAGGTTTGGGCGCGGATCCGGAGCTGAGCGGGCGGCACCCCTCTCTCTGTC	120	
Db	61	CAAGGTTTGGGCGCGGATCCGGAGCTGAGCGGGCGGCACCCCTCTCTCTGTC	120	
QY	121	GGTCACAGCAATGTACGGCTCGGCTGGCTGCCCTCCCGCAGGATTCCCATCCCA	180	

[illegible]

Db	1201	CTGAGCGCGACACGGCCCCGGACGCTGACCGACATCGAGCAGAAAGTCCAGCGCTACAGC	1261
Qy	1261	CAGCAGCTGGCGAAGGTCCAGGAGGAGCCAGATCCTGCAGGAGCGGTGGCTGAAACC	1320
Db	1261	CAGCAGCTGGCGAAGGTCCAGGAGGAGCCAGATCCTGCAGGAGCGGTGGCTGAAACC	1320
Qy	1321	GACCGCACACCTTCTGGCTGGGTGGCTCTCACTGTCCGAGCGGTCAAGGAAAAATC	1380
Db	1321	GACCGCACACCTTCTGGCTGGGTGGCTCTCACTGTCCGAGCGGTCAAGGAAAAATC	1380
Qy	1381	CATGAGCAACCTCACATATGAGACTTCCCGACCTTCCAAGTACACAGGCCCCCTGCAG	1440
Db	1381	CATGAGCAACCTCACATATGAGACTTCCCGACCTTCCAAGTACACAGGCCCCCTGCAG	1440
Qy	1441	TACACCATCTGGAAGTCCCTGTTCCAGGACATCCACCAGTGCAGCGCCCTAACCCCTG	1500
Db	1441	TACACCATCTGGAAGTCCCTGTTCCAGGACATCCACCAGTGCAGCGCCCTAACCCCTG	1500
Qy	1501	GACCGGGCACAGCCACAGCGCTGATCCTGTCCGACGACTGCACCATTTGGCTTAC	1560
Db	1501	GACCGGGCACAGCCACAGCGCTGATCCTGTCCGACGACTGCACCATTTGGCTTAC	1560
Qy	1561	GGCAACTTGCACCAACAGCCACTGCAGGACTCGCCAAAGCGTTCGATGTGGAGTGTGCG	1620
Db	1561	GGCAACTTGCACCAACAGCCACTGCAGGACTCGCCAAAGCGTTCGATGTGGAGTGTGCG	1620
Qy	1621	GTGCTGGGTCTGAAGCTTCACTAGTGGCGTCCACTTCTGGGAGTGTGTGGGGGAG	1680
Db	1621	GTGCTGGGTCTGAAGCTTCACTAGTGGCGTCCACTTCTGGGAGTGTGTGGGGGAG	1680
Qy	1681	AAGACCCAGTGGGTGATCGGCTGGCACAGAAAGCCGCAAGCGCCAGGCGAGCATCCAG	1740
Db	1681	AAGACCCAGTGGGTGATCGGCTGGCACAGAAAGCCGCAAGCGCCAGGCGAGCATCCAG	1740
Qy	1741	ATCCAGCCAGCGCGGCTTCTACTGCATCGTGTGATGACGATGGCAACAGTACAGGCC	1800
Db	1741	ATCCAGCCAGCGCGGCTTCTACTGCATCGTGTGATGACGATGGCAACAGTACAGGCC	1800
Qy	1801	TGCACGAGCCCTGCAGCGGCTTAAAGTCCGGGACAAGCTTGACAAGTGGGTGTCTTC	1860
Db	1801	TGCACGAGCCCTGCAGCGGCTTAAAGTCCGGGACAAGCTTGACAAGTGGGTGTCTTC	1860
Qy	1861	CTGGACTATGACCAAGGCTTGTCTATCTTACAAATGCTGATGACATGTCTGGCTCTAC	1920
Db	1861	CTGGACTATGACCAAGGCTTGTCTATCTTACAAATGCTGATGACATGTCTGGCTCTAC	1920
Qy	1921	ACCTTCGCGAGAGTTCCTGGCAGCTGTGCTTACTTTCAGCCCTGCGCAGAGCCAC	1980
Db	1921	ACCTTCGCGAGAGTTCCTGGCAGCTGTGCTTACTTTCAGCCCTGCGCAGAGCCAC	1980
Qy	1981	GCCAAATGGCAAGACGTTTACGCGCTCGGATCAACACCGTCCGCATCTAGTCCAGGCAG	2040
Db	1981	GCCAAATGGCAAGACGTTTACGCGCTCGGATCAACACCGTCCGCATCTAGTCCAGGCAG	2040
Qy	2041	AAGGAGACCAACCTCTCTGGGACCACTGGCACCTGCAAGAGCCCTGCCAGGAAGTAG	2100
Db	2041	AAGGAGACCAACCTCTCTGGGACCACTGGCACCTGCAAGAGCCCTGCCAGGAAGTAG	2100
Qy	2101	AAGACCTGGACTCCAGGCCACCGTGGCCACTGGAGACTCAGGCCAGTGTTCACCTCC	2160
Db	2101	AAGACCTGGACTCCAGGCCACCGTGGCCACTGGAGACTCAGGCCAGTGTTCACCTCC	2160
Qy	2161	AGCCTCCAGTCTGTAAATGGAGGTTCGATTCCTTCCCTACTTCTTAACTCTCTTCAGCATC	2220
Db	2161	AGCCTCCAGTCTGTAAATGGAGGTTCGATTCCTTCCCTACTTCTTAACTCTCTTCAGCATC	2220
Qy	2221	GATGTTCTGTAGTCTGACCTTGTATAGGGATACAGCTTTGATCCAAAGATGTGACATGGC	2280
Db	2221	GATGTTCTGTAGTCTGACCTTGTATAGGGATACAGCTTTGATCCAAAGATGTGACATGGC	2280
Qy	2281	TTCTCCTCAGGGAACCCCTGCCCAACCCCTCATCCCATCTTCTCAGGGGAGGGGACTA	2340
Db	2281	TTCTCCTCAGGGAACCCCTGCCCAACCCCTCATCCCATCTTCTCAGGGGAGGGGACTA	2340


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; LENGTH: 4702
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-295-027-141

Query Match      0.7%; Score 26; DB 16; Length 4702;
Best Local Similarity 100.0%; Pred. No. 0.049;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3801 GATGTCACAAAAA 3826
Db 4660 GATGTCACAAAAA 4685

RESULT 3
US-10-295-027-1164
; Sequence 1164, Application US/10295027
; Publication No. US20030232350A1
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsberg, Wendy M.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Glynn, Richard
; APPLICANT: Hevezi, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Murray, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; FILE REFERENCE: 018501-012500US
; CURRENT APPLICATION NUMBER: US/10/295,027
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 09/663,733
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/335,394
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/332,464
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/334,393
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: US 60/340,376
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/347,211
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 60/347,349
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/355,250
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 60/356,714
; PRIOR FILING DATE: 2002-02-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1386
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1164
; LENGTH: 4702
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-295-027-1164
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Query Match      0.7%; Score 26; DB 16; Length 4702;
Best Local Similarity 100.0%; Pred. No. 0.049;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3801 GATGTCACAAAAA 3826
Db 4660 GATGTCACAAAAA 4685

RESULT 4
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US-10-437-963-100661/c
; Sequence 100661, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 100661
; LENGTH: 2511
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_98356C.1
US-10-437-963-100661

Query Match      0.7%; Score 25; DB 17; Length 2511;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3802 ATGTCACAAAAA 3826
Db 26 ATGTCACAAAAA 2

RESULT 5
US-09-745-763-39
; Sequence 39, Application US/09745763
; Patent No. US20020065394A1
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; McCoy, John M.
; Lavallie, Edward R.
; Collins-Racie, Lisa A.
; Evans, Cheryl
; Merberg, David
; Treacy, Maurice
; Spaulding, Vikki
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
; ENCODING THEM
; NUMBER OF SEQUENCES: 219
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/09/745,763
; FILING DATE: 18-Jun-2000
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Sprunger, Suzanne A.
; REGISTRATION NUMBER: 41,323
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8284
; TELEFAX: (617) 876-5851
```



```
/ INFORMATION FOR SEQ ID NO: 39:
/ SEQUENCE CHARACTERISTICS:
/   LENGTH: 2522 base pairs
/   TYPE: nucleic acid
/   STRANDEDNESS: double
/   TOPOLOGY: linear
/ MOLECULE TYPE: cDNA
/ SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-09-745-763-39

Query Match          0.7%; Score 25; DB 9; Length 2522;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3802 ATGTCACAAAAA... 3826
Db 2495 ATGTCACAAAAA... 2519

RESULT 6
US-10-104-047-875/c
/ Sequence 875, Application US/10104047
/ Publication No. US20030236392A1
/ GENERAL INFORMATION:
/ APPLICANT: HELIX RESEARCH INSTITUTE
/ TITLE OF INVENTION: No. US20030236392A1el full length cDNA
/ FILE REFERENCE: HI-A0105
/ CURRENT APPLICATION NUMBER: US/10/104,047
/ CURRENT FILING DATE: 2002-03-25
/ PRIOR APPLICATION NUMBER:
/ PRIOR FILING DATE:
/ NUMBER OF SEQ ID NOS: 4096
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 875
/ LENGTH: 2586
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/
US-10-104-047-875

Query Match          0.7%; Score 25; DB 16; Length 2586;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3802 ATGTCACAAAAA... 3826
Db 2112 ATGTCACAAAAA... 2088

RESULT 7
US-10-106-698-1916
/ Sequence 1916, Application US/10106698
/ Publication No. US20030109690A1
/ GENERAL INFORMATION:
/ APPLICANT: Ruben et al.
/ TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide
/ FILE REFERENCE: PA005P1
/ CURRENT APPLICATION NUMBER: US/10/106,698
/ CURRENT FILING DATE: 2002-03-27
/ PRIOR APPLICATION NUMBER: PCT/US00/26524
/ PRIOR FILING DATE: 2000-09-28
/ PRIOR APPLICATION NUMBER: US 60/157,137
/ PRIOR FILING DATE: 1999-09-29
/ PRIOR APPLICATION NUMBER: US 60/163,280
/ PRIOR FILING DATE: 1999-11-03
/ NUMBER OF SEQ ID NOS: 8564
/ SOFTWARE: PatentIn Ver. 3.0
/ SEQ ID NO 1916
/ LENGTH: 2629
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (35)..(35)
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/ OTHER INFORMATION: n equals a,t,g, or c
US-10-106-698-1916

Query Match          0.7%; Score 25; DB 15; Length 2629;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3802 ATGTCACAAAAA... 3826
Db 2567 ATGTCACAAAAA... 2591

RESULT 8
US-09-529-063-51
/ Sequence 51, Application US/09529063
/ Patent No. US20020102542A1
/ GENERAL INFORMATION:
/ APPLICANT: FUKUSHIMA, DAIKICHI
/ APPLICANT: SHIBAYAMA, SHIRO
/ APPLICANT: TADA, HIDEAKI
/ TITLE OF INVENTION: POLYPEPTIDE, cDNA ENCODING THE POLYPEPTIDE, AND USE OF
/ TITLE OF INVENTION: THE BOTH
/ FILE REFERENCE: Q58769
/ CURRENT APPLICATION NUMBER: US/09/529,063
/ CURRENT FILING DATE: 2000-04-07
/ PRIOR APPLICATION NUMBER: PCT/JP98/04514
/ PRIOR FILING DATE: 1998-10-06
/ PRIOR APPLICATION NUMBER: JP 9-274674
/ PRIOR FILING DATE: 1997-10-07
/ NUMBER OF SEQ ID NOS: 117
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 51
/ LENGTH: 2796
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: sig_peptide
/ LOCATION: (11)..(58)
/ NAME/KEY: mat_peptide
/ LOCATION: (59)..(1273)
/ NAME/KEY: CDS
/ LOCATION: (11)..(1273)
/
US-09-529-063-51

Query Match          0.7%; Score 25; DB 9; Length 2796;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3802 ATGTCACAAAAA... 3826
Db 2768 ATGTCACAAAAA... 2792

RESULT 9
US-10-414-378-51
/ Sequence 51, Application US/10414378
/ Publication No. US20030165981A1
/ GENERAL INFORMATION:
/ APPLICANT: FUKUSHIMA, DAIKICHI
/ APPLICANT: SHIBAYAMA, SHIRO
/ APPLICANT: TADA, HIDEAKI
/ TITLE OF INVENTION: POLYPEPTIDE, cDNA ENCODING THE POLYPEPTIDE, AND USE OF
/ TITLE OF INVENTION: THE BOTH
/ FILE REFERENCE: Q58769
/ CURRENT APPLICATION NUMBER: US/10/414,378
/ CURRENT FILING DATE: 2003-04-16
/ PRIOR APPLICATION NUMBER: US/09/529,063
/ PRIOR FILING DATE: 2000-04-07
/ PRIOR APPLICATION NUMBER: PCT/JP98/04514
/ PRIOR FILING DATE: 1998-10-06
/ PRIOR APPLICATION NUMBER: JP 9-274674
/ PRIOR FILING DATE: 1997-10-07
/ NUMBER OF SEQ ID NOS: 117
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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 51
; LENGTH: 2796
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: (11)..(58)
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: (59)..(1273)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (11)..(1273)
; US-10-414-378-51

Query Match 0.7%; Score 25; DB 15; Length 2796;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3802 ATGTCAAAAAAAAAAAAAAAAAAAAA 3826
|||||
DB 2768 ATGTCAAAAAAAAAAAAAAAAAAAAA 2792

RESULT 10

US-10-424-599-137631
; Sequence 137631, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 137631
; LENGTH: 2806
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_9528C.1
US-10-424-599-137631

Query Match 0.7%; Score 25; DB 13; Length 2806;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3802 ATGTCAAAAAAAAAAAAAAAAAAAAA 3826
|||||
DB 2455 ATGTCAAAAAAAAAAAAAAAAAAAAA 2479

RESULT 11

US-10-615-659-11
; Sequence 11, Application US/10615659
; Publication No. US20040157234A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING A NOVEL TESTIS-SPECIFIC TUBULIN
; FILE REFERENCE: D0283 NP
; CURRENT APPLICATION NUMBER: US/10/615,659
; CURRENT FILING DATE: 2003-07-09
; PRIOR APPLICATION NUMBER: U.S. 60/394,725
; PRIOR FILING DATE: 2002-07-09
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 11

; LENGTH: 3465
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-615-659-11

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Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3802 ATGTCAAAAAAAAAAAAAAAAAAAAA 3826
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DB 3441 ATGTCAAAAAAAAAAAAAAAAAAAAA 3465

RESULT 12

US-10-437-963-54840
; Sequence 54840, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barthazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 54840
; LENGTH: 3504
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_56905C.1
US-10-437-963-54840

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Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3802 ATGTCAAAAAAAAAAAAAAAAAAAAA 3826
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RESULT 13

US-10-615-659-12
; Sequence 12, Application US/10615659
; Publication No. US20040157234A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING A NOVEL TESTIS-SPECIFIC TUBULIN
; FILE REFERENCE: D0283 NP
; CURRENT APPLICATION NUMBER: US/10/615,659
; CURRENT FILING DATE: 2003-07-09
; PRIOR APPLICATION NUMBER: U.S. 60/394,725
; PRIOR FILING DATE: 2002-07-09
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 12
; LENGTH: 3554
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-615-659-12

Query Match 0.7%; Score 25; DB 17; Length 3554;
Best Local Similarity 100.0%; Pred. No. 0.16;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Job time : 1155 secs

RESULT 14

US-10-450-826-108

; Sequence 108, Application US/10450826

; Publication No. US20040101818A1

; GENERAL INFORMATION:

; APPLICANT: Ji, Darren

; APPLICANT: Axelrod, Douglas W.

; APPLICANT: Cook, Jonathon S.

; APPLICANT: Jaiswal, Neelam

; APPLICANT: Eistein, Richard

; APPLICANT: Houghton, Adam

; APPLICANT: Mertz, Lawrence

; TITLE OF INVENTION: Gene Expression Profiles Associated with Osteoblast Differentiation

; FILE REFERENCE: 044921-5039-WO

; CURRENT APPLICATION NUMBER: US/10/450,826

; CURRENT FILING DATE: 2003-06-18

; PRIOR APPLICATION NUMBER: US 60/255,882

; PRIOR FILING DATE: 2000-12-18

; PRIOR APPLICATION NUMBER: US 60/285,691

; PRIOR FILING DATE: 2001-04-24

; NUMBER OF SEQ ID NOS: 149

; SOFTWARE: Patentin Ver. 2.1

; SEQ ID NO 108

; LENGTH: 4572

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; OTHER INFORMATION: Genbank Accession No. AK000465

US-10-450-826-108

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Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3802 ATGTCACAAAAA 3826
 Db 4548 ATGTCACAAAAA 4572

RESULT 15

US-09-945-265-3

; Sequence 3, Application US/09945265

; Patent No. US20020123614A1

; GENERAL INFORMATION:

; APPLICANT: Springer, Timothy A.

; APPLICANT: Shimaoka, Motomu

; APPLICANT: Lu, Chafen

; TITLE OF INVENTION: MODIFIED POLYPEPTIDES STABILIZED IN A

; FILE REFERENCE: CHN-002CP

; CURRENT APPLICATION NUMBER: US/09/945,265

; CURRENT FILING DATE: 2001-08-31

; PRIOR APPLICATION NUMBER: US 60/229,700

; PRIOR FILING DATE: 2000-09-01

; NUMBER OF SEQ ID NOS: 4

; SOFTWARE: Fast-Seq for Windows Version 4.0

; SEQ ID NO 3

; LENGTH: 4740

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-945-265-3

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Best Local Similarity 100.0%; Pred. No. 0.15; Indels 0; Gaps 0;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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GenCore version 5.1.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 4, 2004, 08:24:02 : Search time 6095 Seconds
(without alignments)

18745.316 Million cell updates/sec

Title: US-09-927-091-3

Perfect score: 3826

Sequence: 1 aggcgcctggaccgaagc.....aaaaaaaaaaaaaaaaaaaaa 3826

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Word size : 18

Total number of hits satisfying chosen parameters: 3147

Minimum DB seq length: 2500

Maximum DB seq length: 5000

Post-processing: Listing first 45 summaries

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5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_htc:*

9: gb_est1:*

10: gb_est2:*

11: gb_htc:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: em_gss_hum:*

18: em_gss_inv:*

19: em_gss_pln:*

20: em_gss_vrt:*

21: em_gss_fun:*

22: em_gss_man:*

23: em_gss_mus:*

24: em_gss_pro:*

25: em_gss_rod:*

26: em_gss_pbg:*

27: em_gss_vrl:*

28: gb_gss1:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	25	0.7	3080	BC037619	BC037619 Mus muscu
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4	24	0.6	2963	AK085089	AK085089 Mus muscu

5	24	0.6	3234	11	AK081017	AK081017 Mus muscu
6	24	0.6	3250	11	BC035530	BC035530 Mus muscu
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8	24	0.6	3444	11	BC039604	BC039604 Homo sapi
9	24	0.6	3707	13	C83838	C83838 C3838 Dict
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11	24	0.6	4168	11	BC042403	BC042403 Mus muscu
12	24	0.6	4207	11	BC034315	BC034315 Homo sapi
13	23	0.6	2669	11	BC035179	BC035179 Homo sapi
14	23	0.6	2752	11	BC014615	BC014615 Homo sapi
15	23	0.6	2802	11	BC030311	BC030311 Mus muscu
16	23	0.6	2819	11	BC051011	BC051011 Mus muscu
17	23	0.6	2860	11	BC043612	BC043612 Homo sapi
18	23	0.6	2907	11	BC024884	BC024884 Mus muscu
19	23	0.6	2911	11	AK090089	AK090089 Mus muscu
20	23	0.6	2942	11	AK090144	AK090144 Mus muscu
21	23	0.6	2970	11	BC023335	BC023335 Mus muscu
22	23	0.6	2978	11	BC030337	BC030337 Mus muscu
23	23	0.6	3066	11	AK040164	AK040164 Mus muscu
24	23	0.6	3089	11	AK079444	AK079444 Mus muscu
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26	23	0.6	3109	11	AK039198	AK039198 Mus muscu
27	23	0.6	3266	11	BC035538	BC035538 Mus muscu
28	23	0.6	3301	11	AK029761	AK029761 Mus muscu
29	23	0.6	3395	11	BC033458	BC033458 Mus muscu
30	23	0.6	3444	11	BC008551	BC008551 Mus muscu
31	23	0.6	3466	11	AK052111	AK052111 Mus muscu
32	23	0.6	3741	11	BC034973	BC034973 Homo sapi
33	23	0.6	3814	11	BC016415	BC016415 Mus muscu
34	23	0.6	4042	11	BC052704	BC052704 Mus muscu
35	23	0.6	4585	11	BC059828	BC059828 Mus muscu
36	23	0.6	4617	11	BC007668	BC007668 Homo sapi
37	23	0.6	4619	11	BC058338	BC058338 Mus muscu
38	22	0.6	2504	11	BC011059	BC011059 Mus muscu
39	22	0.6	2507	11	AK048762	AK048762 Mus muscu
40	22	0.6	2509	11	BC036220	BC036220 Homo sapi
41	22	0.6	2512	11	BC036441	BC036441 Homo sapi
42	22	0.6	2520	11	AK086585	AK086585 Mus muscu
43	22	0.6	2521	11	BC049779	BC049779 Mus muscu
44	22	0.6	2527	11	BC042136	BC042136 Homo sapi
45	22	0.6	2528	11	AF451985	AF451985 Homo sapi

ALIGNMENTS

RESULT 1
AK048725
LOCUS
DEFINITION
Mus musculus 0 day neonate cerebellum cDNA, RIKEN full-length enriched library, clone:C230023D16 product:similar to CDNA FLJ10759 FIS, CLONE NT2RP3004617, WEAKLY SIMILAR TO ZINC-BINDING PROTEIN A33 [Homo sapiens], full insert sequence.

ACCESSION
AK048725

VERSION
AK048725.1 GI:26093070

KEYWORDS
HTC; CAP trapper.

SOURCE
Mus musculus (house mouse)

ORGANISM
Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

REFERENCE
1

Carninci, P. and Hayashizaki, Y.

High-efficiency full-length cDNA cloning

Meth. Enzymol. 303, 19-44 (1999)

99279253

PUBMED
10349636

REFERENCE
2

Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,

Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.

Normalization and subtraction of cap-trapper-selected cDNAs to

prepare full-length cDNA libraries for rapid discovery of new genes

Genome Res. 10 (10), 1617-1630 (2000)

20499374

```

PUBMED
REFERENCE
AUTHORS
11042159
3 Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
Konno,H., Akiyama,J., Nishi,K., Kitsuai,T., Tashiro,H., Itoh,M.,
Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
Yanamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
Fujiwaki,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
Okazaki,Y., Muramatsu,M., Inoue,Y., Kita,A. and Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multipillar sequencer
Genome Res. 10 (11), 1757-1771 (2000)
20530913
MEDLINE
PUBMED
11076861
4 The RIKEN Genome Exploration Research Group Phase II Team and the
FANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
5 The FANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 2726)
Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T.,
Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T.,
Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,
Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,
Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N.,
Okazaki,Y., Saito,K., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N.,
Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
Segabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
Muramatsu,M. and Hayashizaki,Y.
Direct Submission
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.go.jp,
URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222,
Fax: 81-45-503-9216)
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL: http://genome.gsc.riken.go.jp/
URL: http://fantom.gsc.riken.go.jp/.
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DEFINITION Mus musculus, clone IMAGE:5400144, mRNA.
ACCESSION BC037619
VERSION BC037619.1 GI:22902286
KEYWORDS HTC.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Strausberg,R.
Direct Submission
Submitted (13-SEP-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: gcapbs-remail.nih.gov
Tissue Procurement: The Cepko Laboratory
cDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland
Web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov
Akhtar,N., Ayale,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Tsurgueon,C., Vogt,J.L., Walker,N.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,E.D.
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAC Plate: 81 Row: p Column: 13
This clone was selected for full length sequencing because it
passed the following selection criteria: Hexamer frequency ORF
analysis, GenomeScan gene prediction
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Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps C;

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JOURNAL Nature 420, 563-573 (2002)
REFERENCE 6 (bases 1 to 2963)
AUTHORS Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,
Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,
Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,
Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,
Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,
Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N.,
Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,
Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,
Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,
Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
Muramatsu, M. and Hayashizaki, Y.
TITLE Direct Submission
JOURNAL Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.go.jp,
URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222,
Fax: 81-45-503-9216)
COMMENT cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL: http://genome.gsc.riken.go.jp/
URL: http://fantom.gsc.riken.go.jp/
FEATURES
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|||||
Db 24 TGTCAAAAAAAAAAAAAAAAAAAAAA 1
RESULT 5
LOCUS AK081017 3234 bp mRNA linear HTC 20-SEP-2003
DEFINITION Mus musculus 10 days neonate cerebellum cDNA, RIKEN full-length
inserted library, clone:B930054008 product:unclassified, full
insert sequence.
ACCESSION AK081017
VERSION AK081017.1 GI:26099613
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1
REFERENCE Carninci, P. and Hayashizaki, Y.
AUTHORS High-efficiency full-length cDNA cloning
TITLE Meth. Enzymol. 303, 19-44 (1999)
JOURNAL 99279253
MEDLINE

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10349636

PUBMED
REFERENCE
AUTHORS

Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)

20499374

MEDLINE
PUBMED

Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
Konno, H., Akiyama, J., Nishi, K., Kitsuina, T., Tashiro, H., Itoh, M.,
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanuki, M.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)

20530913

MEDLINE
PUBMED

The RIKEN Genome Exploration Research Group Phase II Team and the
FANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)

11076861

REFERENCE
AUTHORS

The FANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)

6 (bases 1 to 3234)

JOURNAL
REFERENCE
AUTHORS

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,
Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,
Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,
Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,
Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,
Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N.,
Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,
Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,
Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,
Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
Muramatsu, M. and Hayashizaki, Y.

Direct Submission

TITLE
JOURNAL

Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.go.jp,
URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222,
Fax: 81-45-503-9216)

COMMENT

cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL: http://genome.gsc.riken.go.jp/
URL: http://fantom.gsc.riken.go.jp/.

FEATURES
source

1. .3234
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="FANTOM.DB:B930054008"
/db_xref="MGI:2412933"
/db_xref="taxon:10090"
/clone="B930054008"
/tissue_type="cerebellum"
/clone_lib="RIKEN full-length enriched mouse cDNA library"

```

/dev_stage="10 days neonate"
misc_feature 1..3234
              /note="unclassifiable"

ORIGIN
Query Match      0.6%; Score 24; DB 11; Length 3234;
Best Local Similarity 100.0%; Pred. No. 2.1e+04;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3803 TGTCAAAAAAAAAAAAAAAAAAAAAA 3826
      |||||||||||||||||||||||||||
Db 132 TGTCAAAAAAAAAAAAAAAAAAAAAA 155

RESULT 6
BC035530
LOCUS BC035530 3250 bp mRNA linear HTC 19-NOV-2003
DEFINITION Mus musculus RIKEN cDNA 1200014D22 gene, mRNA (cDNA clone
IMAGE:5366096), with apparent retained intron.
ACCESSION BC035530.1 GI:23242360
VERSION BC035530
KEYWORDS HTC.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 3250)
AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
Diatchenko,L., Marusik,K., Farmer,A.A., Rubin,G.M., Hong,L.,
Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
Scheetz,T.E., Brownstein,M.J., Ustin,T.B., Toshiyuki,S.,
Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
Fahey,J., Helton,E., Kettman,M., Madan,A., Rodrigues,S.,
Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
Butterfield,Y.S., Kravinsky,M.I., Skalska,U., Smalls,D.E.,
Schnerch,A., Schein,J.E., Jones,S.T. and Marra,M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
MEDLINE 22388257
PUBMED 12477932
REFERENCE 2 (bases 1 to 3250)
AUTHORS Strausberg,R.
DIRECT SUBMISSION
TITLE Direct Submission
JOURNAL National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapps-r@mail.nih.gov
Tissue procurement: The Cepko Laboratory
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Contact: nisc.mgc@nih.gov
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,E.D.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK plate: 65 Row: e Column: 18
This clone has the following problem: retained intron.

FEATURES
Location/Qualifiers
1..3250
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:5366096"
/tissue_type="Eye, retina, mouse strain C57Bl/6"
/clone_lib="NIH_MGC_94"
/lab_host="DH10B"
/note="Vector: pCMV-SF0RT6"

ORIGIN
Query Match      0.6%; Score 24; DB 11; Length 3250;
Best Local Similarity 100.0%; Pred. No. 2.1e+04;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3803 TGTCAAAAAAAAAAAAAAAAAAAAAA 3826
      |||||||||||||||||||||||||||
Db 3094 TGTCAAAAAAAAAAAAAAAAAAAAAA 3117

RESULT 7
CA916724
LOCUS CA916724 3415 bp mRNA linear EST 14-MAR-2003
DEFINITION K58FL human keratinocyte matchmaker cDNA library Homo sapiens cDNA
clone K58 5' similar to Arkadia, mRNA sequence.
ACCESSION CA916724
VERSION CA916724.1 GI:28951961
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 3415)
AUTHORS Scarafia,L.E., Stouffer,S.D. and Swimney,D.C.
TITLE Identification of Ring Finger proteins that interact with UbCH5a,
an ubiquitin-conjugating enzyme
JOURNAL Unpublished (2002)
COMMENT Contact: Scarafia LE
Enzymology
Roche Bioscience
3401 Hillview Ave, S3-1, Palo Alto, CA 94304-1397, USA
Tel: 650 354 7997
Fax: 650 354 7554
Email: liliana.scarafia@roche.com
Full length single stranded sequencing of baited insert
Insert length: 3000 Std Error: 0.00
Seg primer: primer 2 (5395)TACCACATCAATGATG; and insert-specific
POLYA=yes.

FEATURES
Location/Qualifiers
1..3415
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="K58"
/cell_type="keratinocyte"
/cell_line="HaCat cell line; derived from long term primary
human adult skin keratinocyte"
/lab_host="yeast/E.coli"
/clone_lib="human keratinocyte matchmaker cDNA library"
/note="Vector: pACT2; Site 1: EcoRI; Site 2: XhoI;
Matchmaker yeast two-hybrid system from Clontech; pACT2
vector has GAL4 AD and HA epitope under ADHI promoter.
This oligo-dT primed library was screened with human
UbCH5a as bait, to obtained interacting proteins."
```

ORIGIN

Query Match 0.6%; Score 24; DB 14; Length 3415;
 Best Local Similarity 100.0%; Pred. No. 2e+04;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3803 TGTCACAAAAA...AAAAAAAAA 3826
 Db 3388 TGTCACAAAAA...AAAAAAAAA 3411

RESULT 8

BC039604
 LOCUS 3444 bp mRNA HTC 04-MAR-2003
 DEFINITION Homo sapiens, clone IMAGE:3847010, mRNA.

ACCESSION BC039604
 VERSION BC039604.1 GI:25058528

KEYWORDS

SOURCE HTC.

ORGANISM

Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 3444)
 Strausberg, R.
 Direct Submission
 Submitted (01-NOV-2002) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA

REMARK

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

COMMENT

Contact: MGC help desk
 Email: cgabs-remail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Institute for Systems Biology
<http://www.systemsbio.org>
 contact: amad@systemsbiology.org
 Anup Madan, Jessica Fahey, Erin Helton, Mark Kettelman, Anuradha
 Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting

Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAC Plate: 84 Row: a Column: 13
 This clone was selected for full length sequencing because it
 passed the following selection criteria: GenomeScan gene prediction
 This clone has the following problem: retained intron.

FEATURES

source

1..3444
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:3847010"
 /tissue_type="Colon, adenocarcinoma"
 /clone_lib="NIH MGC_65"
 /lab_host="DH10B"
 /note="Vector: pCMV-SPORT6"

ORIGIN

Query Match 0.6%; Score 24; DB 11; Length 3444;
 Best Local Similarity 100.0%; Pred. No. 2e+04;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3803 TGTCACAAAAA...AAAAAAAAA 3826
 Db 3419 TGTCACAAAAA...AAAAAAAAA 3442

RESULT 9

BC8388
 LOCUS 3707 bp mRNA linear EST 28-APR-1999
 DEFINITION Dictyostelium discoideum SS (H.Urushihara) Dictyostelium
 discoideum cDNA clone SSA355, mRNA sequence.

ACCESSION

C83838

VERSION

C83838.1 GI:2706770

KEYWORDS

EST.

SOURCE

Dictyostelium discoideum

ORGANISM

Eukaryota; Metazoa; Dictyosteliida; Dictyostelium.
 1 (bases 1 to 3707)
 Morio, T., Urushihara, H., Saito, T., Ugawa, Y., Mizuno, H., Yoshida, M.,
 Yoshino, R., Mitra, B.N., Pi, M., Sato, T., Takemoto, K., Yasukawa, H.,
 Williams, J., Maeda, M., Takeuchi, I., Ochiai, H. and Tanaka, Y.
 The Dictyostelium developmental cDNA project: generation and
 analysis of expressed sequence tags from the first-finger stage of
 development

TITLE

DNA Res. 5 (6), 335-340 (1998)

JOURNAL

99156227

MEDLINE

10048482

PUBMED

COMMENT

Institute: Hideko Urushihara
 Institute of Biological Sciences
 University of Tsukuba
 1-1-1 Tennoudai, Tsukuba, Ibaraki 305-8572, Japan
 Tel: 81-298-53-4664
 Fax: 81-298-53-6614
 Email: hideko@biol.tsukuba.ac.jp
 PROJECT = 'Dictyostelium discoideum cDNA project in Japan'
 POLYA=No.

FEATURES

source

1..3707
 /organism="Dictyostelium discoideum"
 /mol_type="mRNA"
 /strain="AX4"
 /db_xref="taxon:44689"
 /clone="SSA355"
 /dev_stage="slug"
 /clone_lib="Dictyostelium discoideum SS (H.Urushihara)"

ORIGIN

Query Match 0.6%; Score 24; DB 13; Length 3707;
 Best Local Similarity 100.0%; Pred. No. 1.9e+04;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3803 TGTCACAAAAA...AAAAAAAAA 3826

Db 3632 TGTCACAAAAA...AAAAAAAAA 3655

RESULT 10

BC050053

LOCUS

DEFINITION

Homo sapiens DKFZP434I092 protein, mRNA (cDNA clone IMAGE:483930),
 containing frame-shift errors.

ACCESSION

BC050053

VERSION

BC050053.1 GI:29747709

KEYWORDS

HTC.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

REFERENCE

1 (bases 1 to 4097)

AUTHORS

Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
 Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
 Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
 Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
 Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
 Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
 Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
 Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
 Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
 McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
 Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
 Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
 Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodrigues, S.,
 Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
 Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,

Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E., Schnerch, A., Schein, J.E., Jones, S.J., and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
22388257
12477932
2 (bases 1 to 4097)
Strausberg, R.
Direct Submission
Submitted (01-APR-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgaps-remail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center
Center code: BCM-HGSC
Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H., Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati, A.N., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILLNL at: <http://image.llnl.gov>
Series: IRAX Plate: 72 Row: P Column: 7
This clone has the following problem: frame shifted.

FEATURES

source
1. 4097
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4839390"
/tissue_type="Testis"
/clone_lib="NIH MGC_97"
/lab_host="DH10B"
/note="Vector: pBluescript"

ORIGIN

Query Match 0.6%; Score 24; DB 11; Length 4097;
Best Local Similarity 100.0%; Pred. No. 1.7e+04;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3803 TGTCAAAAAAAAAAAAAAAAAAAAAA 3826
Db 4029 TGTCAAAAAAAAAAAAAAAAAAAAAA 4052

RESULT 11

BC042403 4168 bp mRNA linear HTC 19-NOV-2003
LOCUS Mus musculus RIKEN cDNA 1200014D22 gene, mRNA (cDNA clone IMAGE:3156629).
DEFINITION BC042403
ACCESSION BC042403.1 GI:27469394
VERSION
KEYWORDS
SOURCE HPC.
ORGANISM Mus musculus (house mouse)
REFERENCE 1 (bases 1 to 4168)
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,

Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Schetz, T.E., Brownstein, M.J., Uedin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullaly, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettman, M., Maman, A., Rodriguez, S., Sanchez, A., Whitting, M., Madan, A., Young, A.C., Green, E.D., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E., Schnerch, A., Schein, J.E., Jones, S.J., and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
22388257
12477932
2 (bases 1 to 4168)
Strausberg, R.
Direct Submission
Submitted (02-JAN-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgaps-remail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center
Center code: BCM-HGSC
Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H., Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati, A.N., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILLNL at: <http://image.llnl.gov>
Series: IRAX Plate: 61 Row: b Column: 10
This clone has the following problem: no 5' EST match.

FEATURES

source
1. 4168
/organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:3156629"
/tissue_type="Mammary tumor. C3(1)-Tag model. Infiltrating ductal Carcinoma. 5 month old virgin mouse."
/clone_lib="NCI CGAP_Mam6"
/lab_host="DH10B"
/note="Vector: pCMV-SPORT6"

ORIGIN

Query Match 0.6%; Score 24; DB 11; Length 4168;
Best Local Similarity 100.0%; Pred. No. 1.7e+04;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3803 TGTCAAAAAAAAAAAAAAAAAAAAAA 3826
Db 4091 TGTCAAAAAAAAAAAAAAAAAAAAAA 4114

RESULT 12

BC034315
LOCUS
DEFINITION BC034315
Homo sapiens hypothetical protein LOC90529, mRNA (cDNA clone IMAGE:4827425), containing frame-shift errors.

[illegible]

Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

1 (bases 1 to 2752)
 Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullaly, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smal, D.E., Schnerch, A., Schein, J.E., Jones, S.J., and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

12477932

2 (bases 1 to 2752)
 Strausberg, R.
 Direct Submission
 Submitted (24-SEP-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 On Aug 19, 2003 this sequence version replaced gi:15779097.
 Contact: MGC help desk
 Email: cgapsb@mail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Institute for Systems Biology
<http://www.systemsbio.org>
 Contact: amadans@systemsbiology.org
 Anup Madan, Jessica Fahy, Brin Helton, Mark Kettelman, Anuradha Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAL Plate: 11 Row: j Column: 11
 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 18375616
 This clone has the following problem: frame shifted.

FEATURES
 source
 1. .2752
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 /db_xref="taxon:9606"
 /clone="IMAGE:3532298"
 /tissue_type="Muscle, rhabdomyosarcoma"
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 /lab_host="DH10B-R"
 /note="Vector: pOTB7"

ORIGIN
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 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3804 GTCAAAAAAAAAAAAAAAAAAAAAA 3826
 Db 2700 GTCAAAAAAAAAAAAAAAAAAAAAA 2722

RESULT 15
 BC030311

BC030311
 Mus musculus RIKEN cDNA 1200015K23 gene, mRNA (cDNA clone IMAGE:5369232), with apparent retained intron.
 BC030311
 GI:20988454
 HTc
 Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 2802)
 Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullaly, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smal, D.E., Schnerch, A., Schein, J.E., Jones, S.J., and Marra, M.A.

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Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

22388257
 12477932

2 (bases 1 to 2802)
 Strausberg, R.
 Direct Submission
 Submitted (07-MAY-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 Contact: MGC help desk
 Email: cgapsb@mail.nih.gov
 Tissue Procurement: the Cepko Laboratory
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC),
 Gaithersburg, Maryland;
 Web site: <http://www.nisc.nih.gov/>
 Contact: nisc_mgc@hgr.nih.gov
 Akhter, N., Ayelle, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Green, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P., Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Leric, P., Legaspi, R., Maduro, Q.I., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W., Tsurgon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAL Plate: 65 Row: i Column: 23
 This clone has the following problem: retained intron.

FEATURES
 source
 1. .2802
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 /mol_type="mRNA"
 /db_xref="taxon:10090"
 /clone="IMAGE:5369232"
 /tissue_type="Eye, retina, mouse strain C57BL/6"
 /clone_lib="NIH_MGC_94"

/lab_host="DH10B"
/note="Vector: PCMV-SPORT6"

ORIGIN

Query Match 0.6%; Score 23; DB 11; Length 2802;
Best Local Similarity 100.0%; Pred. No. 3.7e+04;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3804 GTCAAAAAAAAAAAAAAAAAAAAA 3826
Db 2778 GTCAAAAAAAAAAAAAAAAAAAAA 2800

Search completed: September 4, 2004, 13:11:20
Job time : 6098 secs